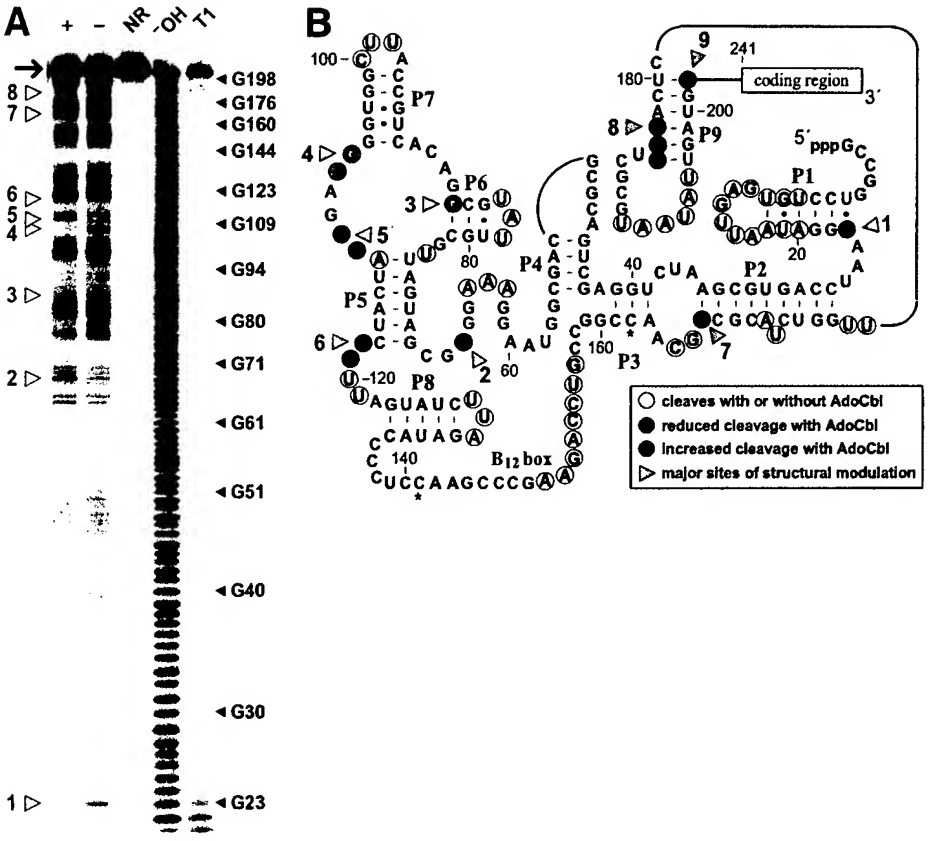

A
+
-
NR
-OH
T1
G198
G176
G160
G144
G123
G109
G94
G80
G71
G61
G51
G40
G30
G23
B
P7
P6
P5
P4
P8
P9
P1
P2
P3
coding region
5'
3'
pppG
B12 box
cleaves with or without AdoCbl
reduced cleavage with AdoCbl
increased cleavage with AdoCbl
major sites of structural modulation

FIG 1

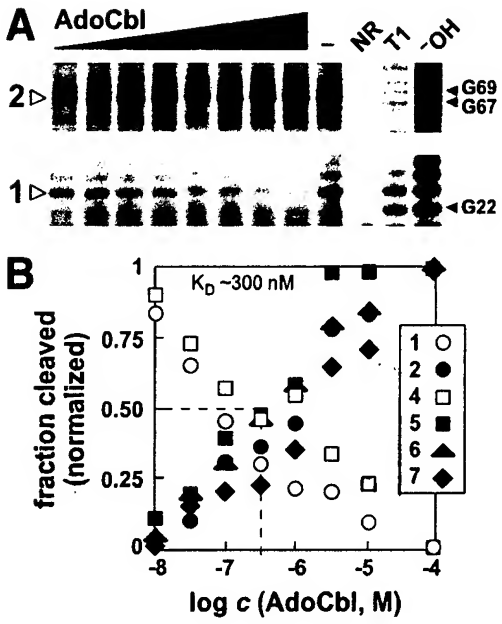

A
AdoCbl
–
NR
T1
-OH
2
G69
G67
1
G22
B
K_D ~300 nM
fraction cleaved (normalized)
1
0.75
0.50
0.25
0
-8
-7
-6
-5
-4
log c (AdoCbl, M)
1
2
4
5
6
7

FIG 2

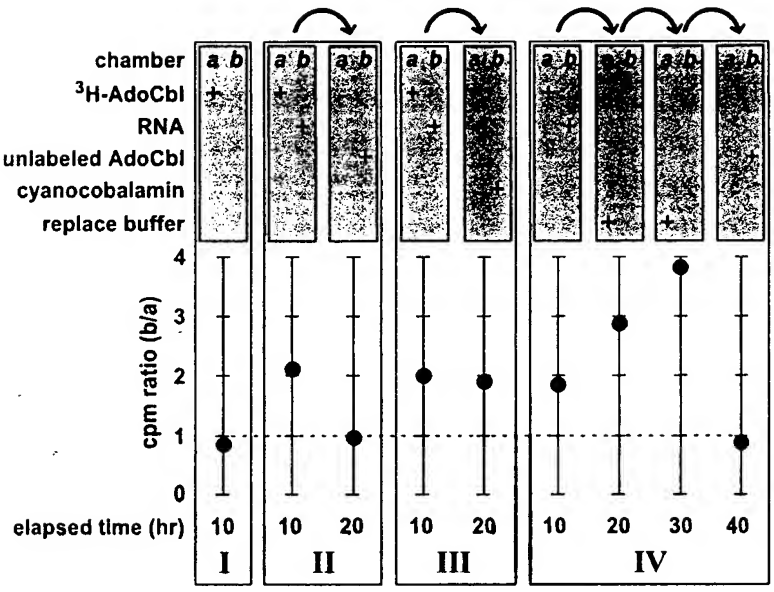

chamber
^{3}H-AdoCbl
RNA
unlabeled AdoCbl
cyanocobalamin
replace buffer
cpm ratio (b/a)
4
3
2
1
0
elapsed time (hr)
10
10
20
10
20
10
20
30
40
I
II
III
IV

FIG 3

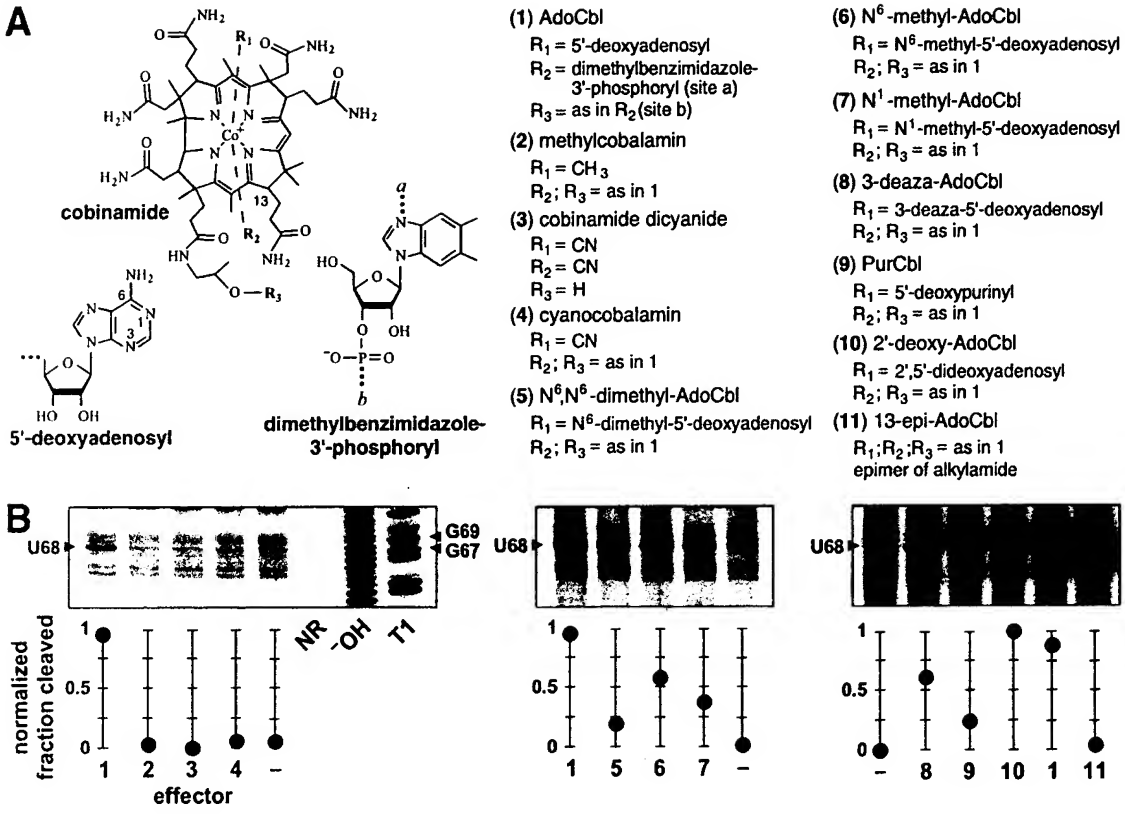

A
cobinamide
5'-deoxyadenosyl
dimethylbenzimidazole-3'-phosphoryl
(1) AdoCbl
R1 = 5'-deoxyadenosyl
R2 = dimethylbenzimidazole-3'-phosphoryl (site a)
R3 = as in R2 (site b)
(2) methylcobalamin
R1 = CH3
R2; R3 = as in 1
(3) cobinamide dicyanide
R1 = CN
R2 = CN
R3 = H
(4) cyanocobalamin
R1 = CN
R2; R3 = as in 1
(5) N6,N6-dimethyl-AdoCbl
R1 = N6-dimethyl-5'-deoxyadenosyl
R2; R3 = as in 1
(6) N6-methyl-AdoCbl
R1 = N6-methyl-5'-deoxyadenosyl
R2; R3 = as in 1
(7) N1-methyl-AdoCbl
R1 = N1-methyl-5'-deoxyadenosyl
R2; R3 = as in 1
(8) 3-deaza-AdoCbl
R1 = 3-deaza-5'-deoxyadenosyl
R2; R3 = as in 1
(9) PurCbl
R1 = 5'-deoxypurinyl
R2; R3 = as in 1
(10) 2'-deoxy-AdoCbl
R1 = 2',5'-dideoxyadenosyl
R2; R3 = as in 1
(11) 13-epi-AdoCbl
R1;R2;R3 = as in 1 epimer of alkylamide
B
U68
G69
G67
NR
-OH
T1
normalized fraction cleaved
effector
1 2 3 4 –
1 5 6 7 –
– 8 9 10 1 11

FIG 4

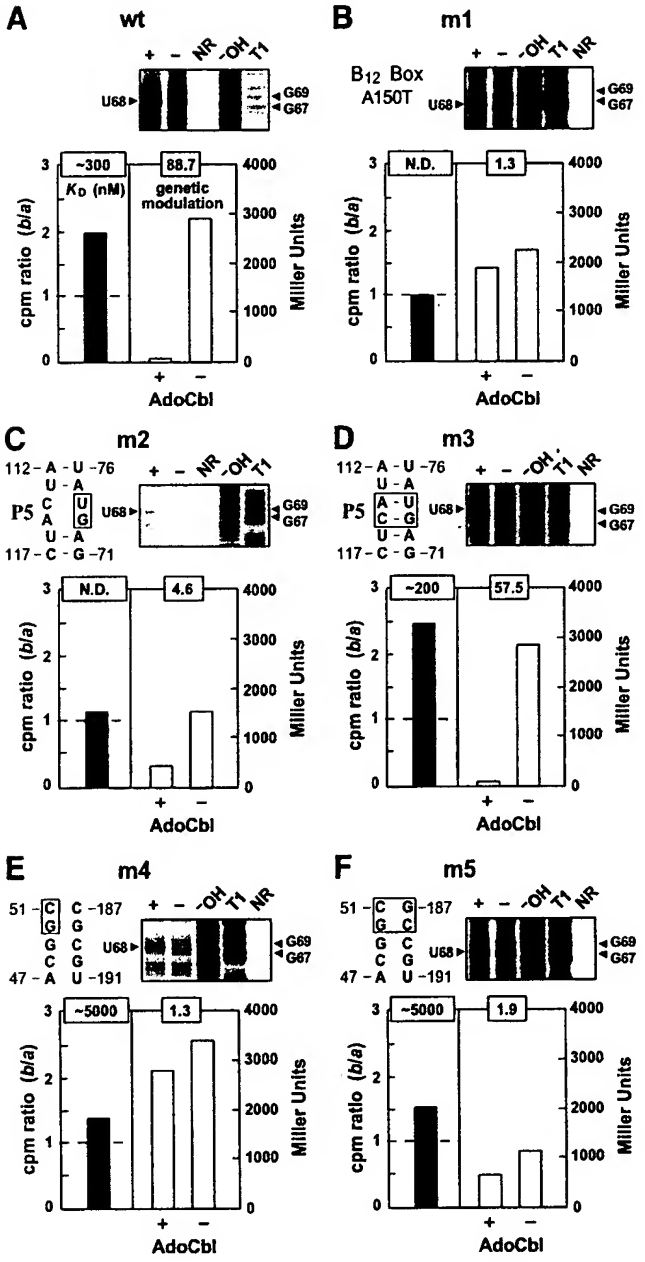

A
wt
+ – NR -OH T1
U68
G69
G67
~300
K_D (nM)
88.7
genetic modulation
cpm ratio (b/a)
Miller Units
AdoCbl
B
m1
B_{12} Box A150T
N.D.
1.3
C
m2
112 – A - U –76
U - A
P5 C U
A G
U - A
117 – C - G –71
4.6
D
m3
A - U
C - G
57.5
~200
E
m4
51 – C C –187
G G
G C
C G
47 – A U –191
~5000
1.3
F
m5
C G
G C
1.9

FIG 5

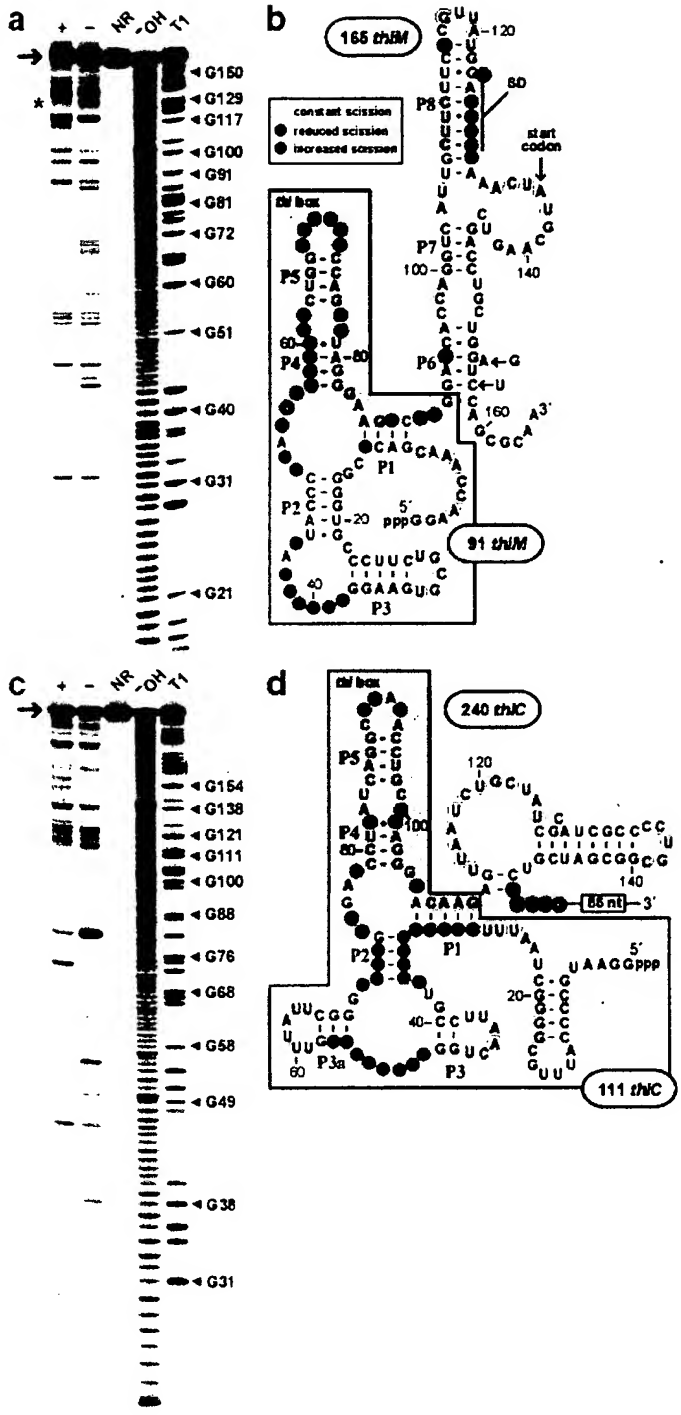

a
+
-
NR
OH
T1
G150
G129
G117
G100
G91
G81
G72
G60
G51
G40
G31
G21
b
165 thiM
constant scission
reduced scission
increased scission
thi box
P5
P4
P8
P7
P6
P1
P2
P3
SD
start codon
91 thiM
c
G154
G138
G121
G111
G100
G88
G76
G68
G58
G49
G38
G31
d
240 thiC
P5
P4
P1
P2
P3a
P3
55 nt
111 thiC

FIG 6

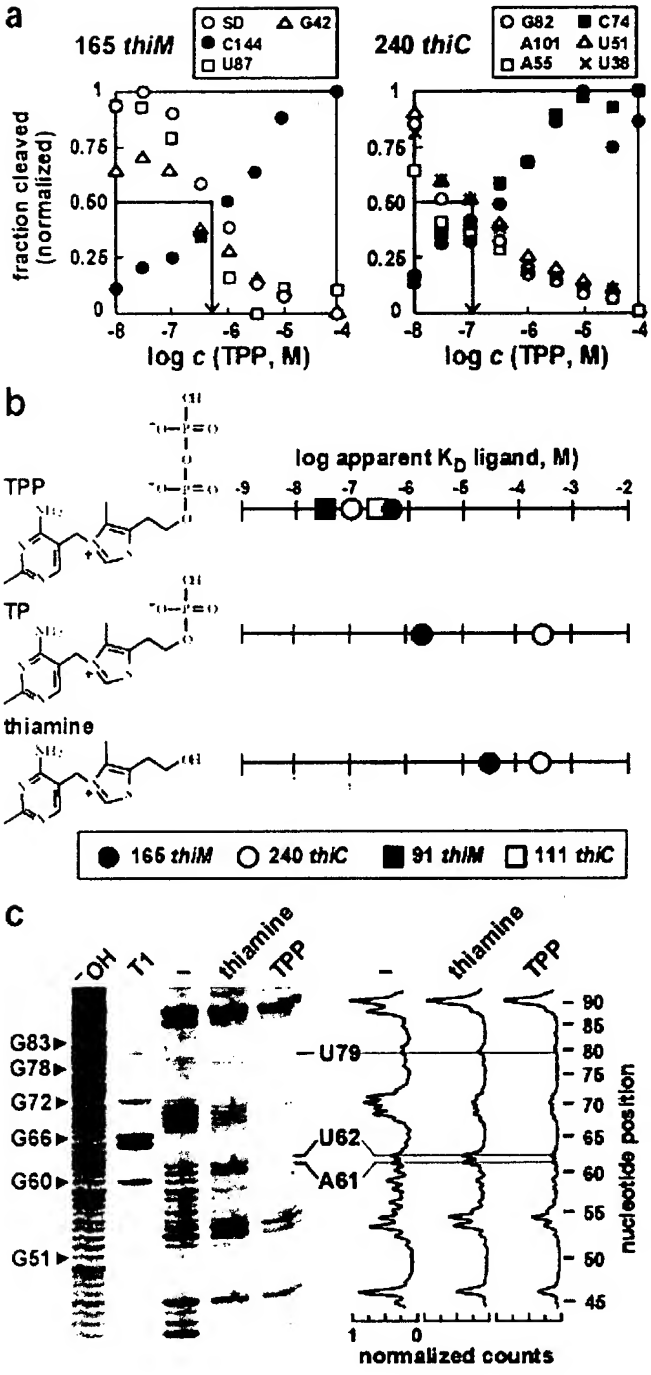

a
165 thiM
SD
G42
C144
U87
240 thiC
G82
C74
A101
U51
A55
U38
fraction cleaved (normalized)
log c (TPP, M)
b
log apparent K_D ligand, M)
TPP
TP
thiamine
165 thiM
240 thiC
91 thiM
111 thiC
c
-OH
T1
thiamine
TPP
G83
G78
G72
G66
G60
G51
U79
U62
A61
nucleotide position
normalized counts

FIG 7

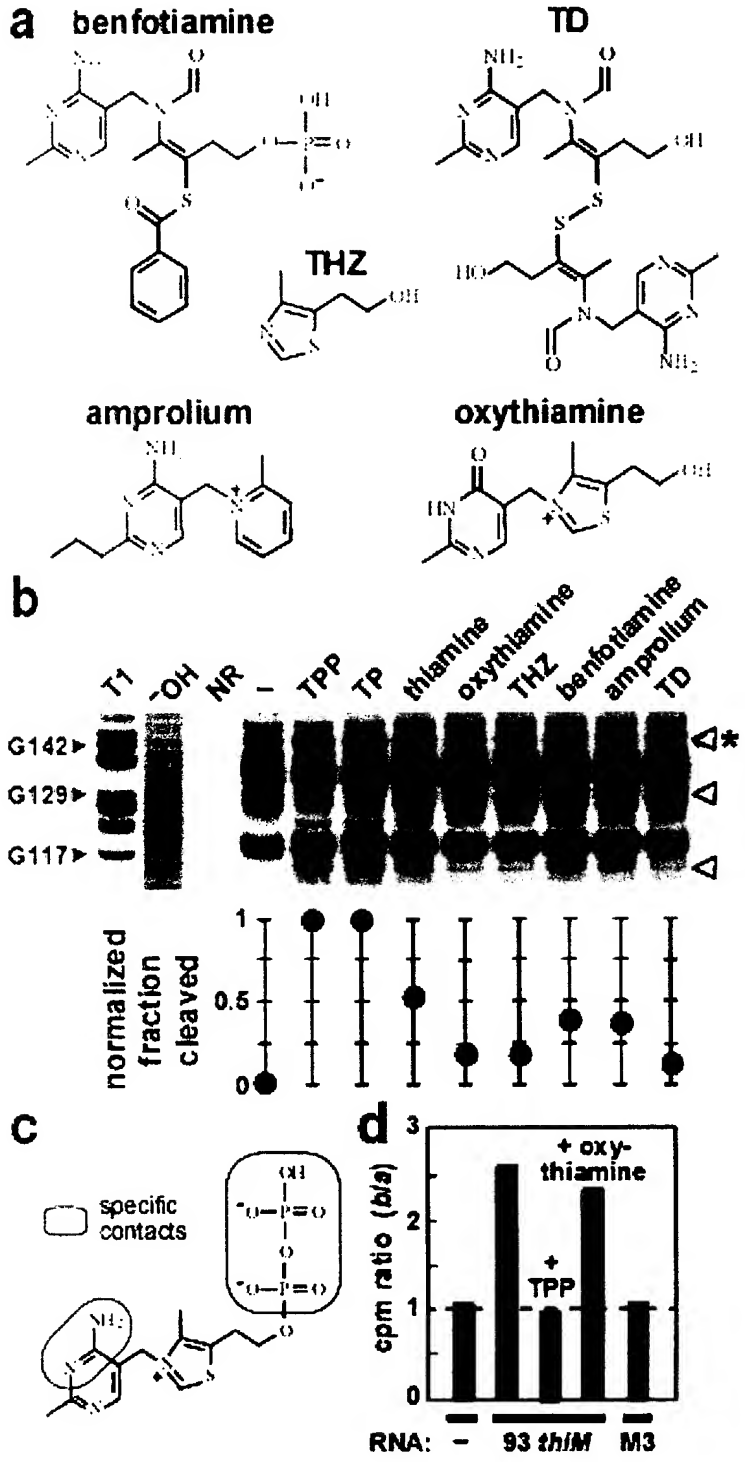
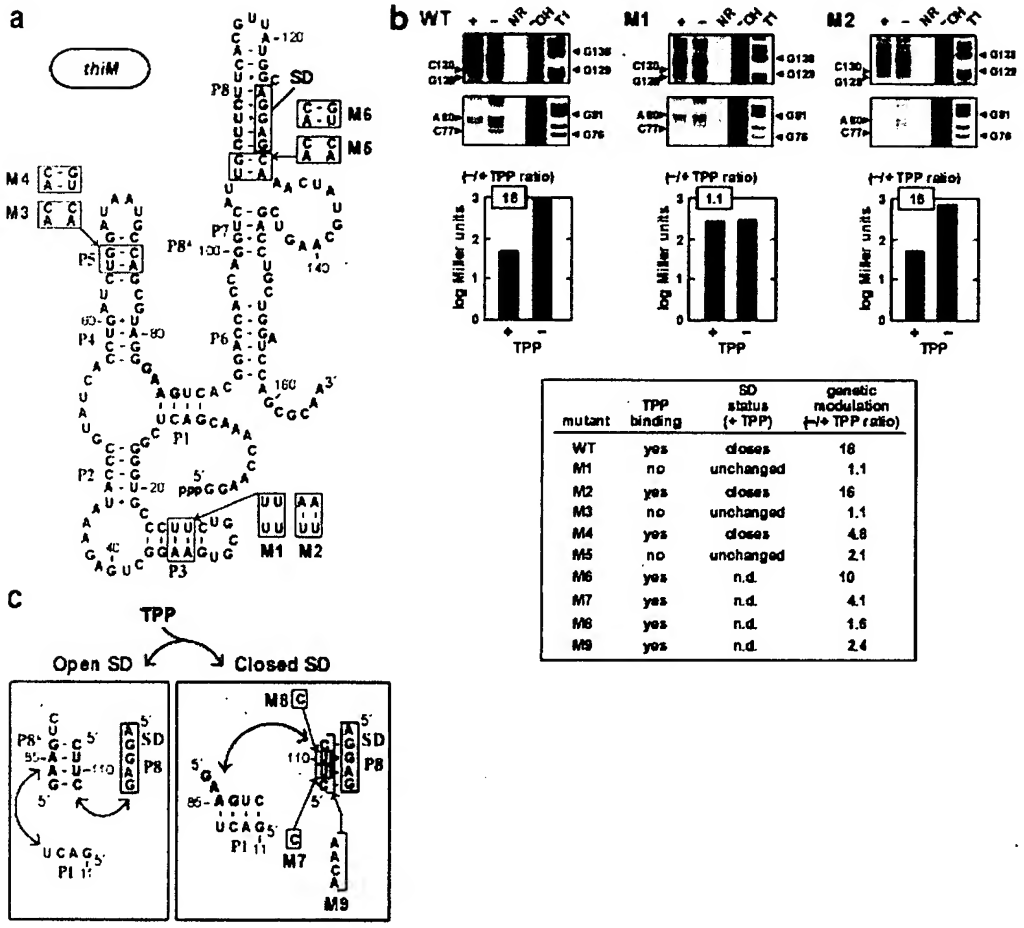

a
benfotiamine
TD
THZ
amprolium
oxythiamine
b
T1
-OH
NR
–
TPP
TP
thiamine
oxythiamine
THZ
benfotiamine
amprolium
TD
G142
G129
G117
*
normalized fraction cleaved
1
0.5
0
c
specific contacts
d
cpm ratio (b/a)
+ oxy-thiamine
+ TPP
3
2
1
0
RNA: – 93 thiM M3

FIG 8



mutant	TPP binding	SD status (+ TPP)	genetic modulation (–/+ TPP ratio)
WT	yes	closes	18
M1	no	unchanged	1.1
M2	yes	closes	16
M3	no	unchanged	1.1
M4	yes	closes	4.8
M5	no	unchanged	2.1
M6	yes	n.d.	10
M7	yes	n.d.	4.1
M8	yes	n.d.	1.6
M9	yes	n.d.	2.4

FIG 9

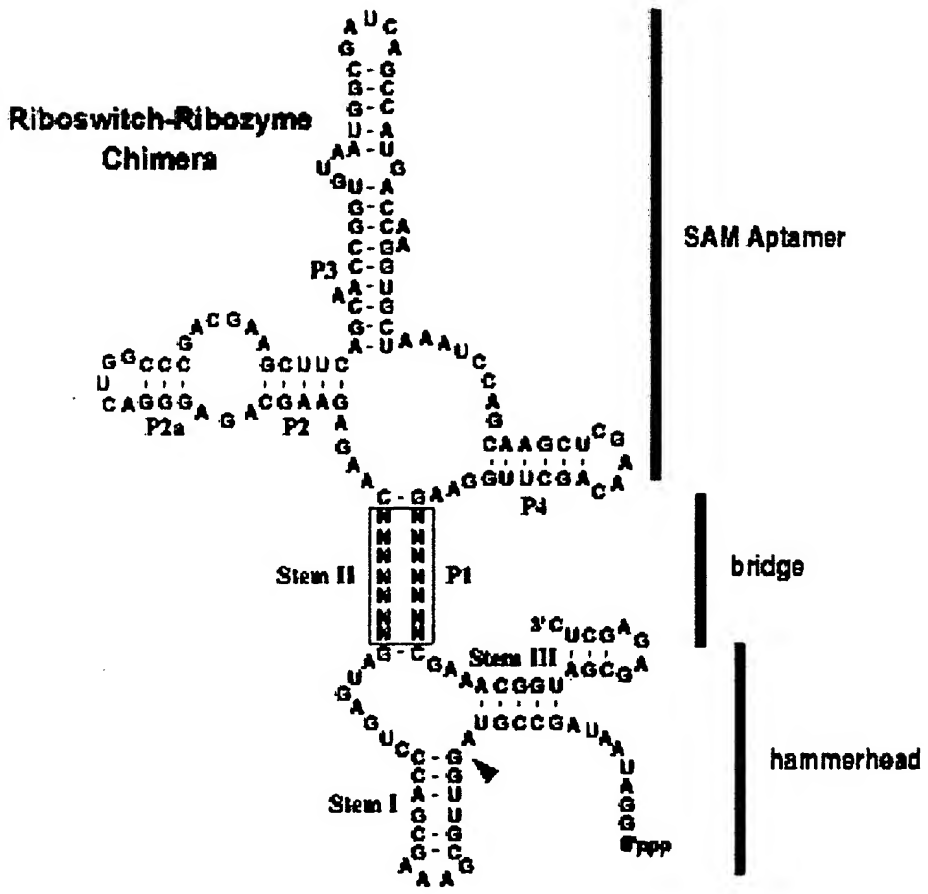

Riboswitch-Ribozyme Chimera
SAM Aptamer
bridge
hammerhead
P3
P2a
P2
P4
Stem II
P1
Stem III
Stem I

FIG 10

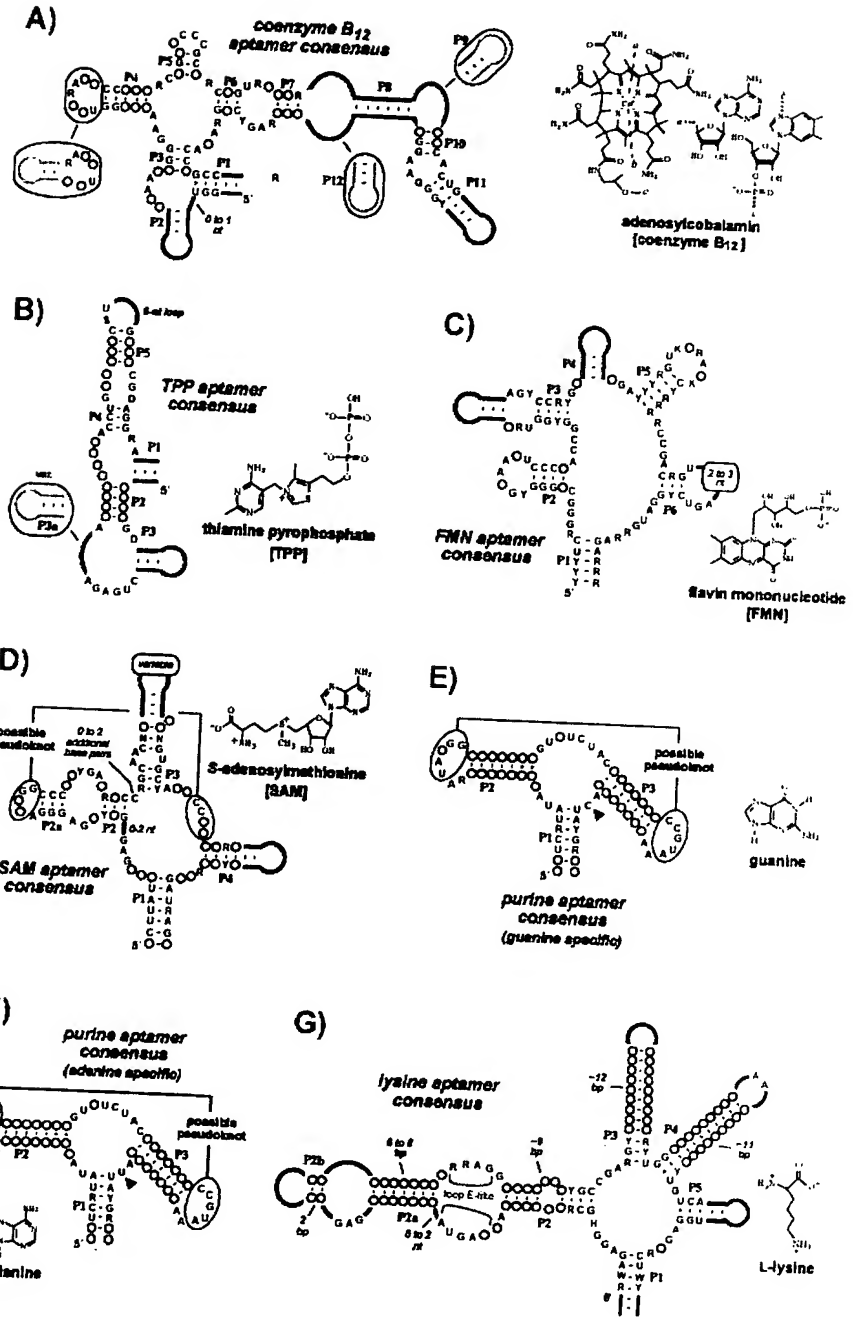

A)
coenzyme B12 aptamer consensus
adenosylcobalamin [coenzyme B12]
B)
TPP aptamer consensus
thiamine pyrophosphate [TPP]
C)
FMN aptamer consensus
flavin mononucleotide [FMN]
D)
possible pseudoknot
S-adenosylmethionine [SAM]
SAM aptamer consensus
E)
possible pseudoknot
guanine
purine aptamer consensus (guanine specific)
F)
purine aptamer consensus (adenine specific)
possible pseudoknot
adenine
G)
lysine aptamer consensus
L-lysine

FIG 11

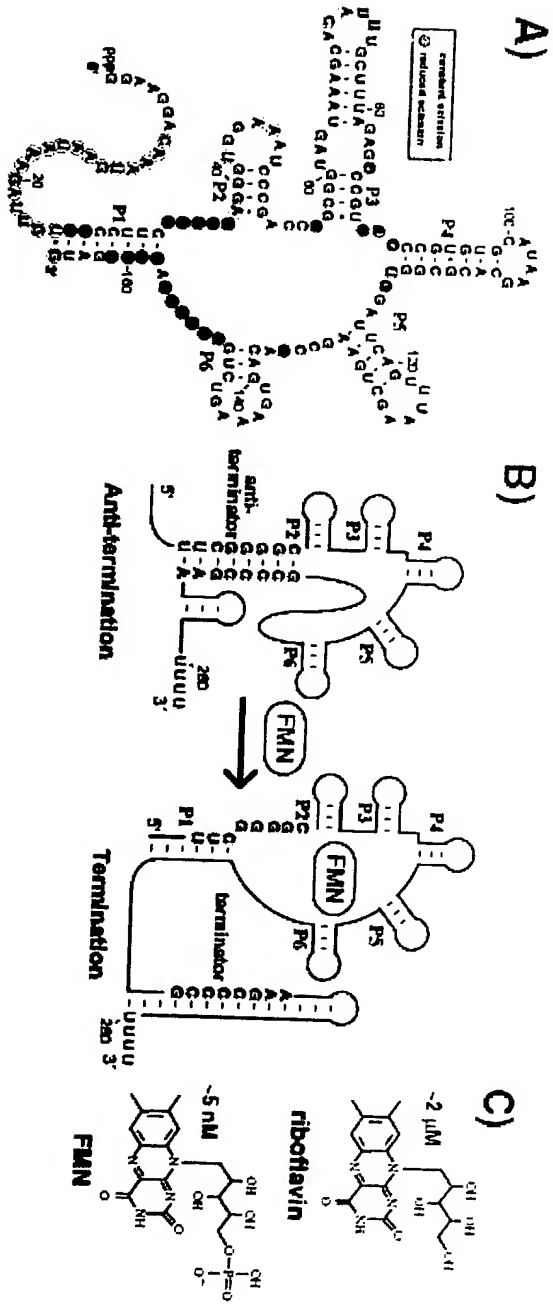

A)
B)
C)
Anti-termination
anti-terminator
Termination
terminator
FMN
-5 nM
FMN
riboflavin
-2 µM

FIG. 12

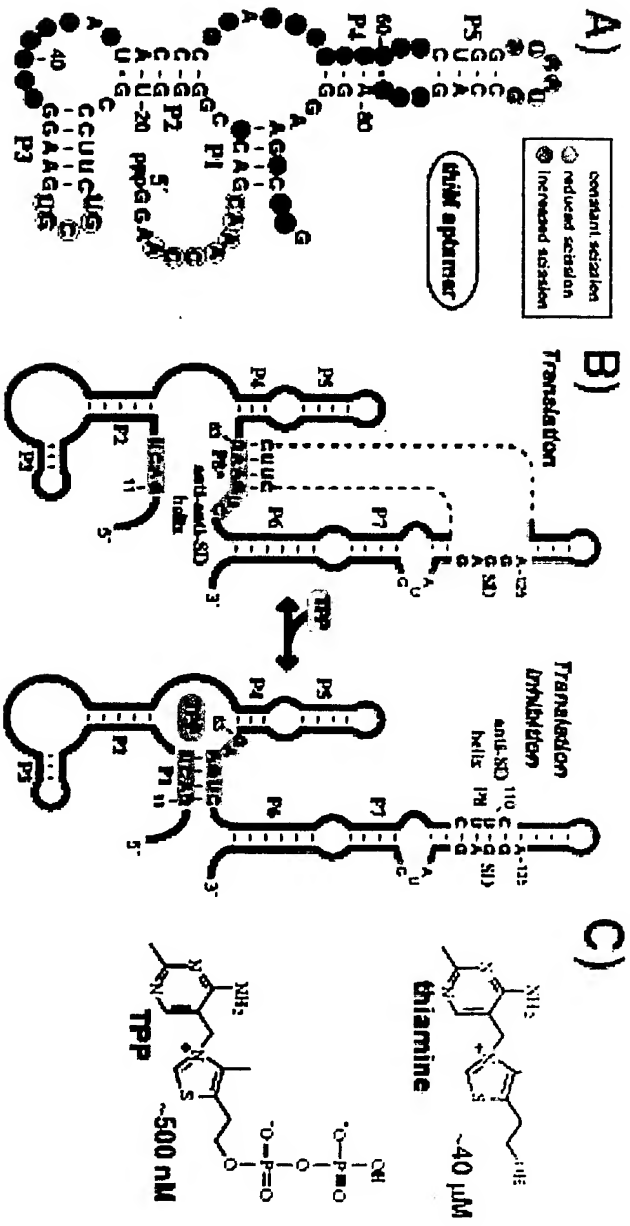

A)
thiM aptamer
constant scission
reduced scission
increased scission
B)
Translation
Translation inhibition
TPP
C)
TPP
~500 nM
thiamine
~40 µM

FIG. 13

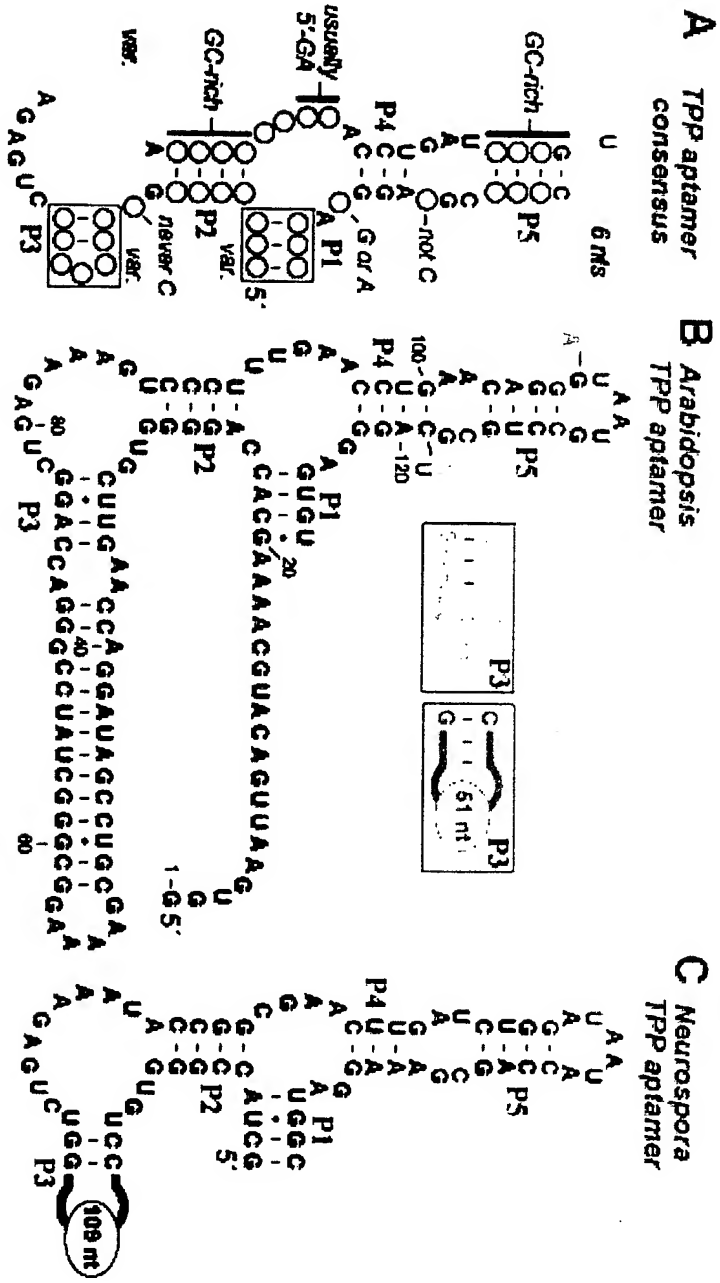

A
TPP aptamer consensus
B
Arabidopsis TPP aptamer
C
Neurospora TPP aptamer
P1
P2
P3
P4
P5
GC-rich
usually 5'-GA
var.
never C
G or A
not C
6 nts
61 nt
109 nt

FIG. 14

ID Position Accession Sequence Name Gene Location
Ecol - 2183973 NC_000913.1 Escherichia coli K12 complete genome thiM operon 5'UTR
Eco2 - 4189775 NC_000913.1 Escherichia coli K12 complete genome thiC operon 5'UTR
Cac - 3156135 NC_003030.1 Clostridium acetobutylicum ATCC824 complete genome thiC 5'UTR
Ner + 664 AY007661.1 Neurospora crassa thiamine biosynthesis protein nmt-1 gene nmt-1 5'UTR Intron
Aor + 622 AF217503.1 Aspergillus oryzae putative thiazole synthase (thiA) gene thiA [thi4] 5'UTR Intron
Fox + 2156 AB033416.1 Fusarium oxysporum sti35 gene for stress-responsive gene product sti35 [thi4] 5'UTR Intron
Fso + 461 M33642.1 Fusarium solani ST135 protein gene sti35 [thi4] 5'UTR Intron
Ath - 78516 AC005496.3 Arabidopsis thaliana chromosome 2 clone T27A16 map mi54 thiamine gene [thiC] 3'UTR
Pse + 2296 AF264021.1 Poa secunda putative thiamine biosynthesis protein ThiC mRNA putative thiC 3'UTR
Osa - 91318 AC084406.7 Oryza sativa chromosome 3 BAC OSJNBa0067E01 genomic sequence putative thiC 3'UTR
P3
P1 P2 P3a P3a P2 P4 P5 P5 P4 P1
Ecol
Eco2
Cacl
Nerl
Aorl
Foxl
Fsol
Athl
Psel
Osal

FIG 15

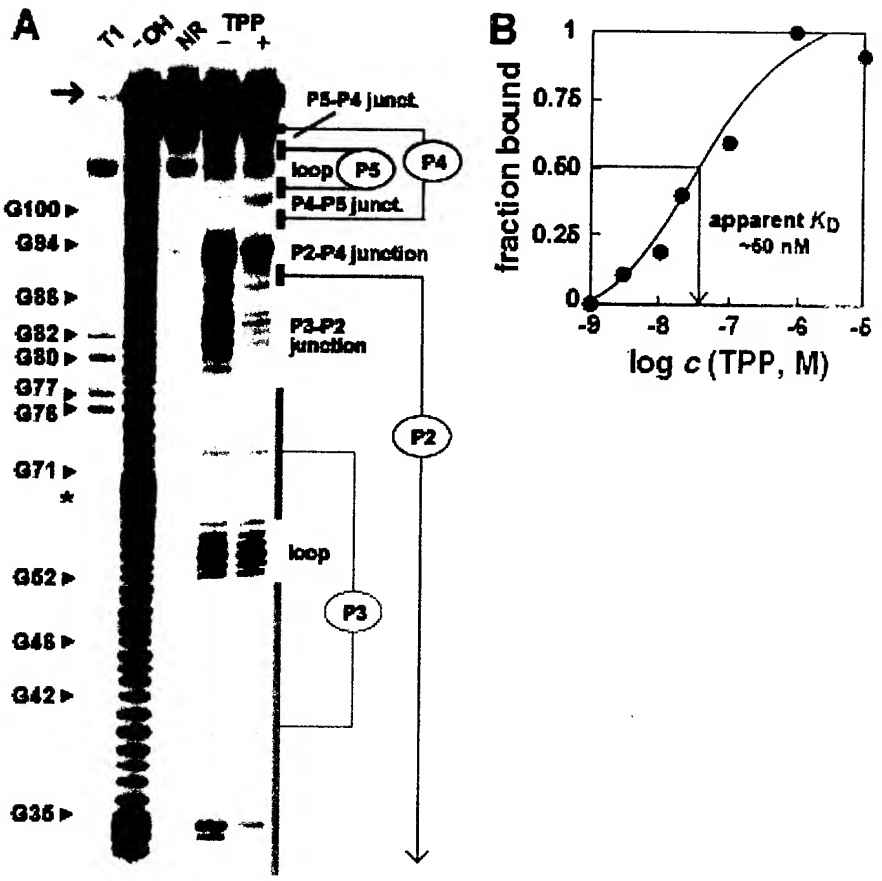

A
T1
-OH
NR
TPP
–
+
P5-P4 junct.
loop
P5
P4
P4-P5 junct.
P2-P4 junction
P3-P2 junction
P2
loop
P3
G100
G94
G88
G82
G80
G77
G76
G71
*
G52
G46
G42
G35
B
fraction bound
1
0.75
0.50
0.25
0
apparent K_D ~50 nM
-9
-8
-7
-6
-5
log c (TPP, M)

FIG 16

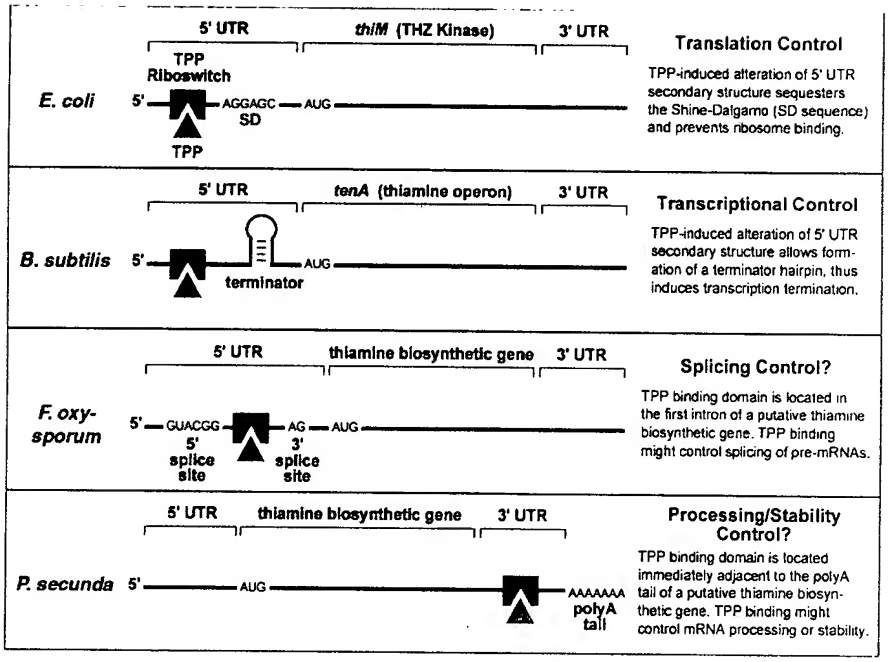

5' UTR
thiM (THZ Kinase)
3' UTR
TPP Riboswitch
E. coli
5'
AGGAGC
AUG
SD
TPP
Translation Control
TPP-induced alteration of 5' UTR secondary structure sequesters the Shine-Dalgarno (SD sequence) and prevents ribosome binding.
5' UTR
tenA (thiamine operon)
3' UTR
B. subtilis
5'
AUG
terminator
Transcriptional Control
TPP-induced alteration of 5' UTR secondary structure allows formation of a terminator hairpin, thus induces transcription termination.
5' UTR
thiamine biosynthetic gene
3' UTR
F. oxysporum
5'
GUACGG
AG
AUG
5' splice site
3' splice site
Splicing Control?
TPP binding domain is located in the first intron of a putative thiamine biosynthetic gene. TPP binding might control splicing of pre-mRNAs.
5' UTR
thiamine biosynthetic gene
3' UTR
P. secunda
5'
AUG
AAAAAAA
polyA tail
Processing/Stability Control?
TPP binding domain is located immediately adjacent to the polyA tail of a putative thiamine biosynthetic gene. TPP binding might control mRNA processing or stability.

FIG 17

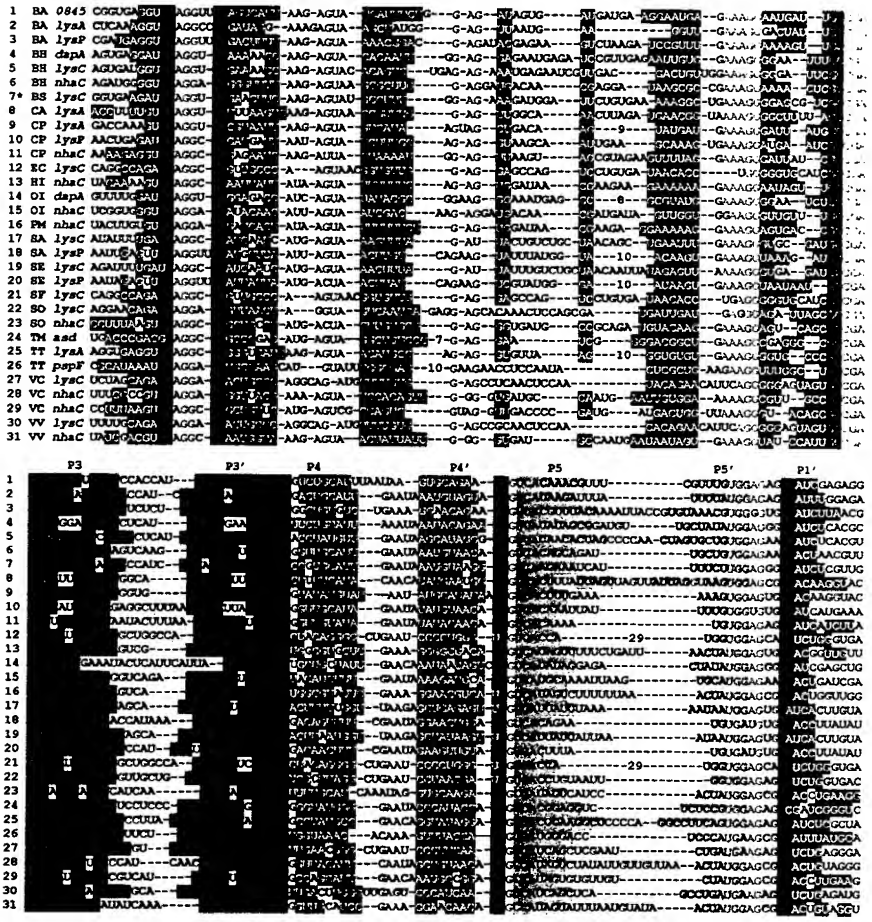


FIG 18

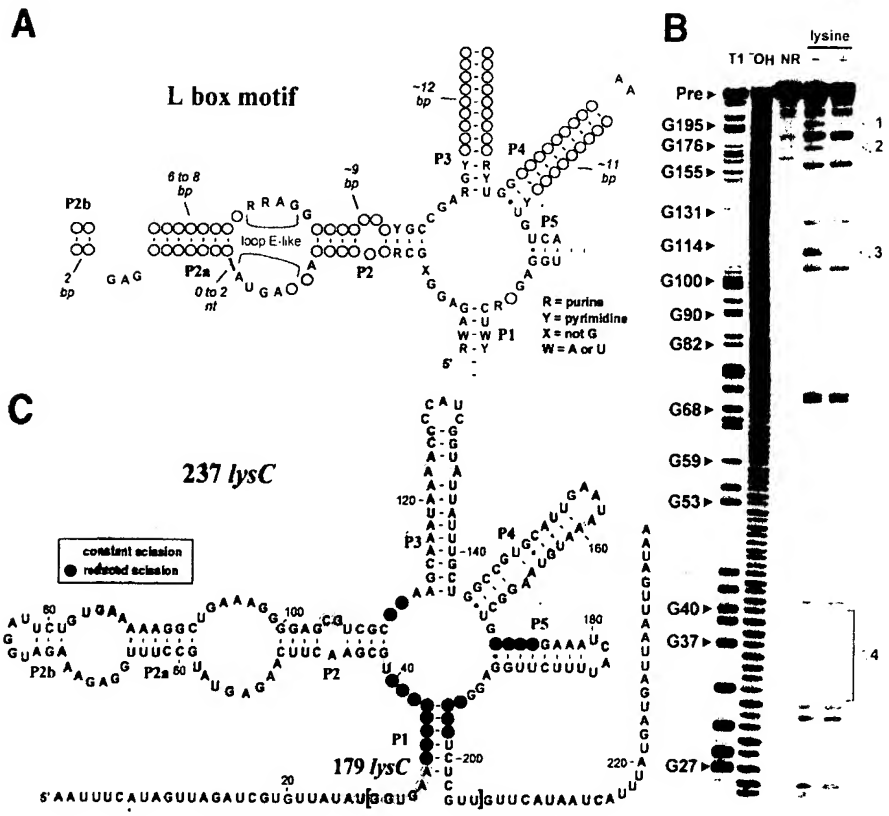

A
L box motif
P2b
P2a
P2
P3
P4
P5
P1
loop E-like
6 to 8 bp
0 to 2 nt
2 bp
~12 bp
~9 bp
~11 bp
R = purine
Y = pyrimidine
X = not G
W = A or U
B
lysine
T1 OH NR
Pre
G195
G176
G155
G131
G114
G100
G90
G82
G68
G59
G53
G40
G37
G27
1
2
3
4
C
237 lysC
179 lysC
constant scission
reduced scission
5'AAUUUCAUAGUUAGAUCGUGUUAUAUUGGUGUUUGUUCAUAAUCAU

FIG. 19

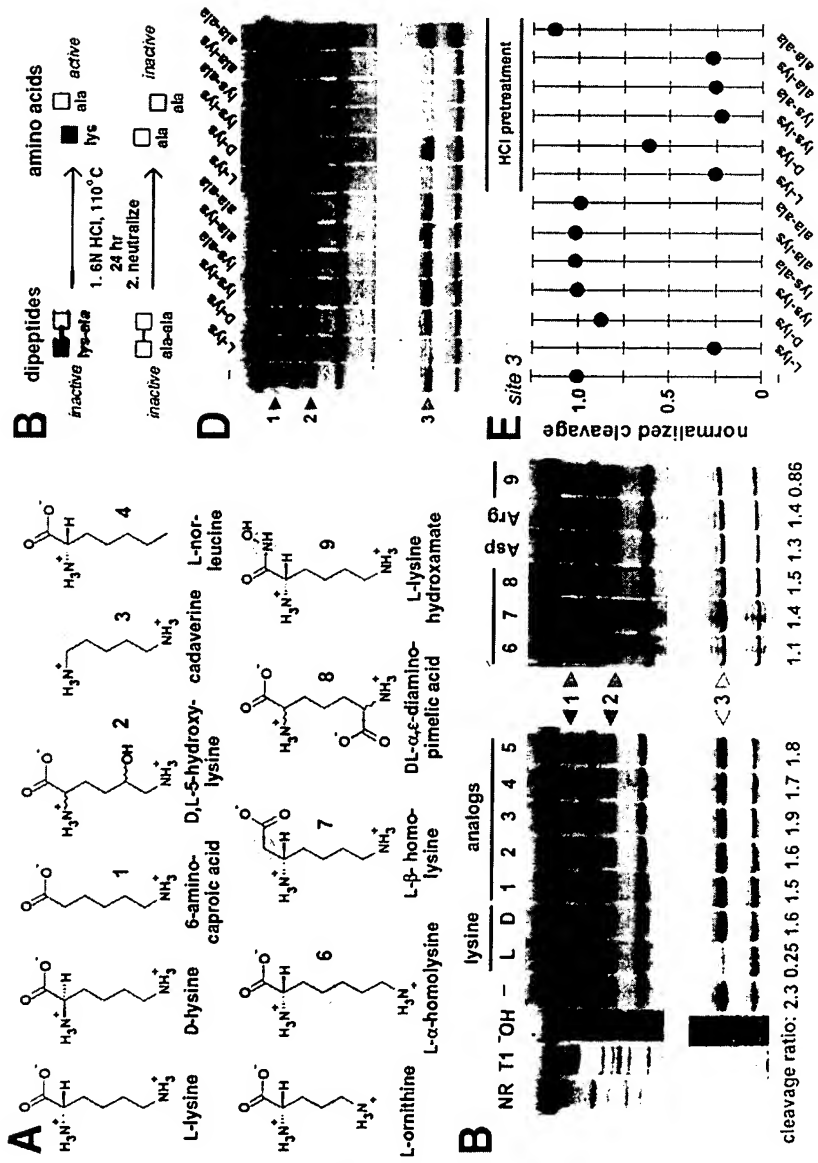

A
L-lysine
D-lysine
L-ornithine
L-α-homolysine
6-amino-caproic acid
L-β- homo-lysine
D,L-5-hydroxy-lysine
DL-α,ε-diamino-pimelic acid
cadaverine
L-nor-leucine
L-lysine hydroxamate
B
dipeptides
amino acids
inactive lys-ala
active ala lys
1. 6N HCl, 110°C 24 hr 2. neutralize
inactive ala-ala
inactive ala ala
D
E
site 3
HCl pretreatment
normalized cleavage
B
NR T1 OH – L D lysine analogs 1 2 3 4 5 6 7 8 Asp 9 Arg
cleavage ratio: 2.3 0.25 1.6 1.5 1.6 1.9 1.7 1.8 1.1 1.4 1.5 1.3 1.4 0.86

FIG. 20

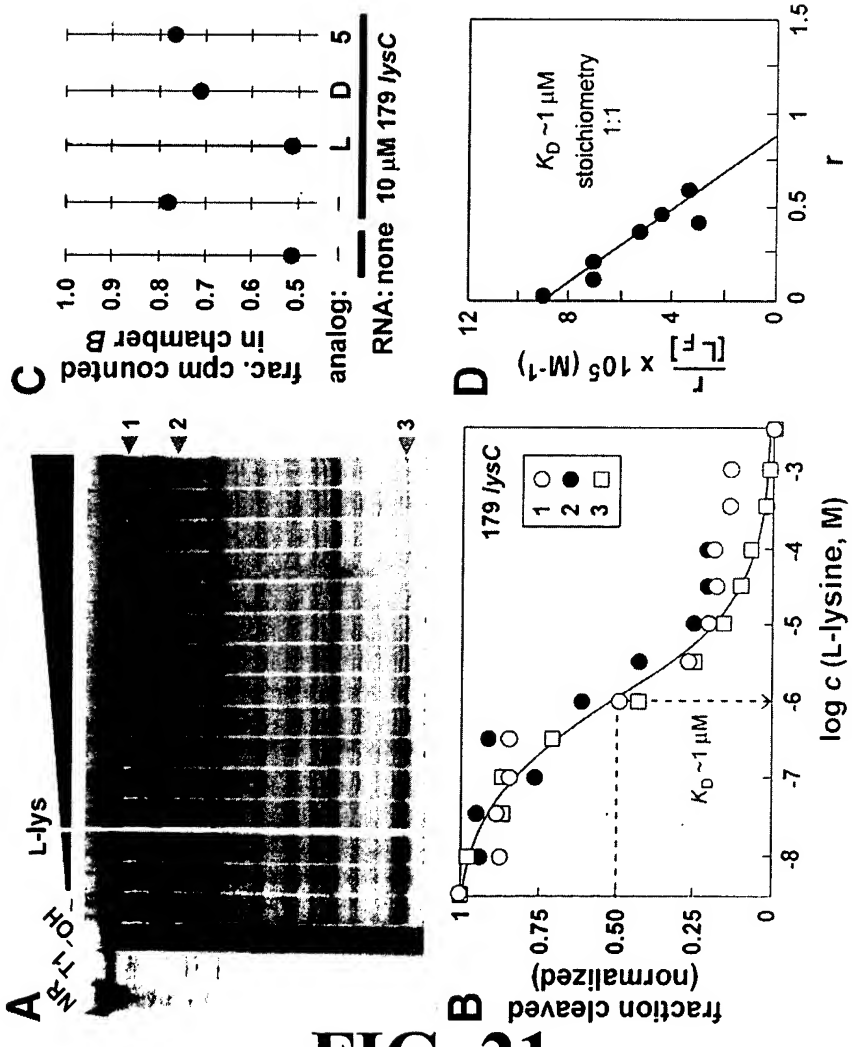

A
NRT_OH
L-lys
1
2
3
B
fraction cleaved (normalized)
179 lysC
1
2
3
K_D ~1 µM
log c (L-lysine, M)
C
frac. cpm counted in chamber B
analog: – – L D 5
RNA: none 10 µM 179 lysC
D
$\frac{r}{[L_F]}$ x 10^5 (M^{-1})
K_D ~1 µM
stoichiometry 1:1
r

FIG 21

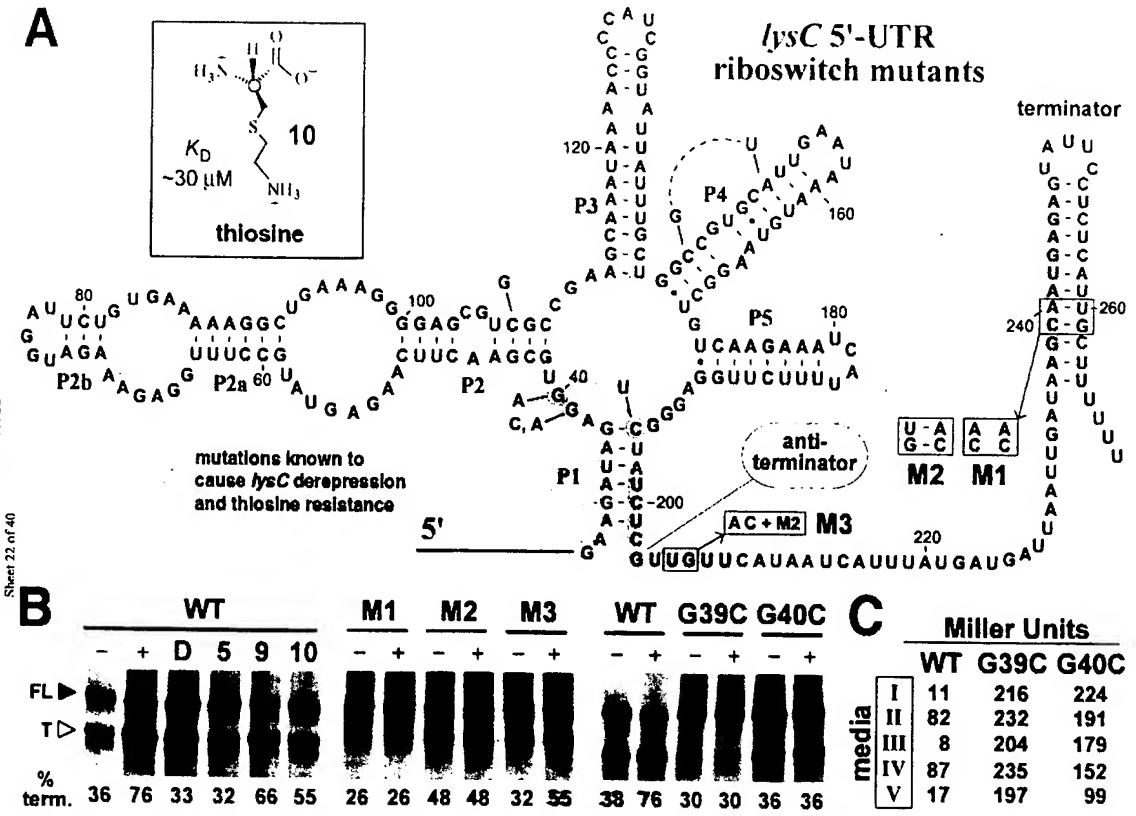

A
thiosine
K_D ~30 µM
10
lysC 5'-UTR riboswitch mutants
terminator
P1
P2
P2a
P2b
P3
P4
P5
anti-terminator
mutations known to cause lysC derepression and thiosine resistance
5'
AC + M2
M3
M2
M1
B
WT
M1
M2
M3
WT
G39C
G40C
– + D 5 9 10
FL
T
% term.
36 76 33 32 66 55
26 26 48 48 32 55
38 76 30 30 36 36
C
Miller Units
media
WT G39C G40C
I 11 216 224
II 82 232 191
III 8 204 179
IV 87 235 152
V 17 197 99

FIG. 22

FIG 23

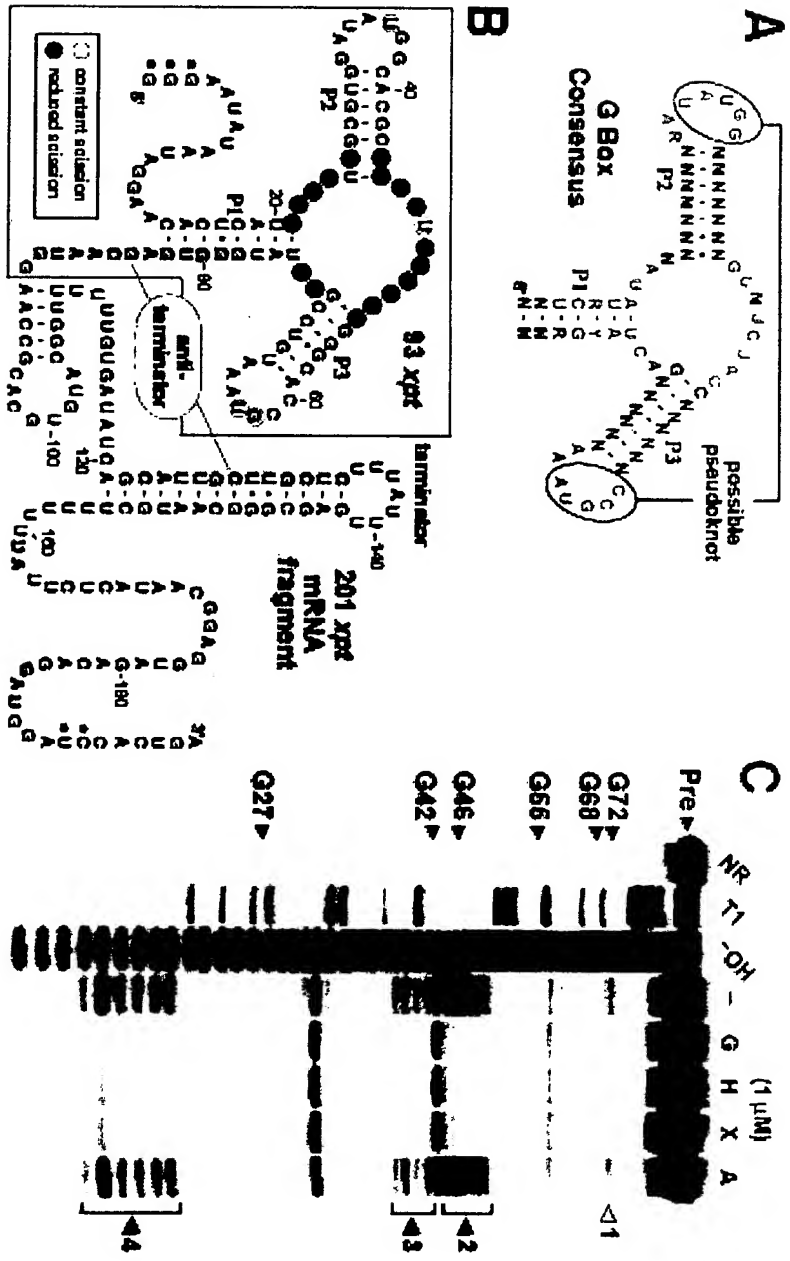

A
G Box Consensus
possible pseudoknot
B
constant scission
reduced scission
anti-terminator
terminator
83 xpt
201 xpt mRNA fragment
C
Pre
G27
G46
G42
G56
G72
G68
NR T1 -OH - G H X A (1 µM)
Δ1
2
3
4

FIG 24

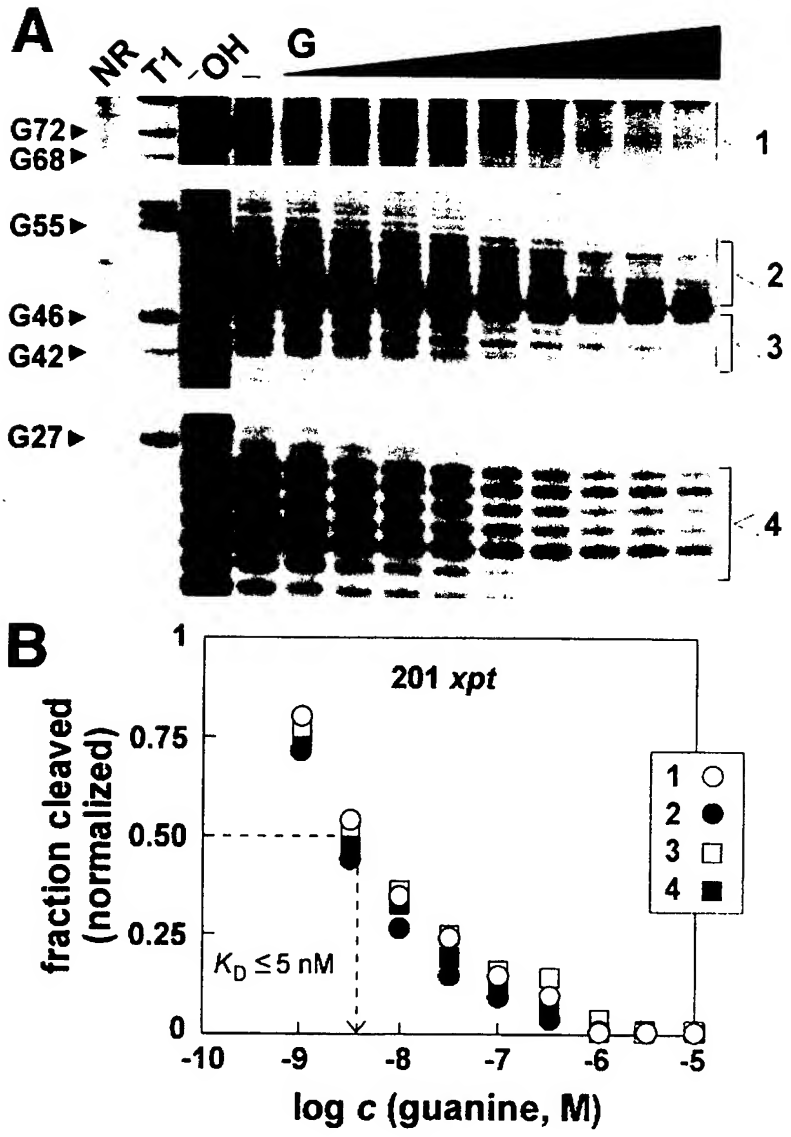

A
NR
T1
OH
G
G72
G68
G55
G46
G42
G27
1
2
3
4
B
201 xpt
fraction cleaved (normalized)
1
0.75
0.50
0.25
0
$K_D \leq 5$ nM
-10
-9
-8
-7
-6
-5
log c (guanine, M)

FIG. 25

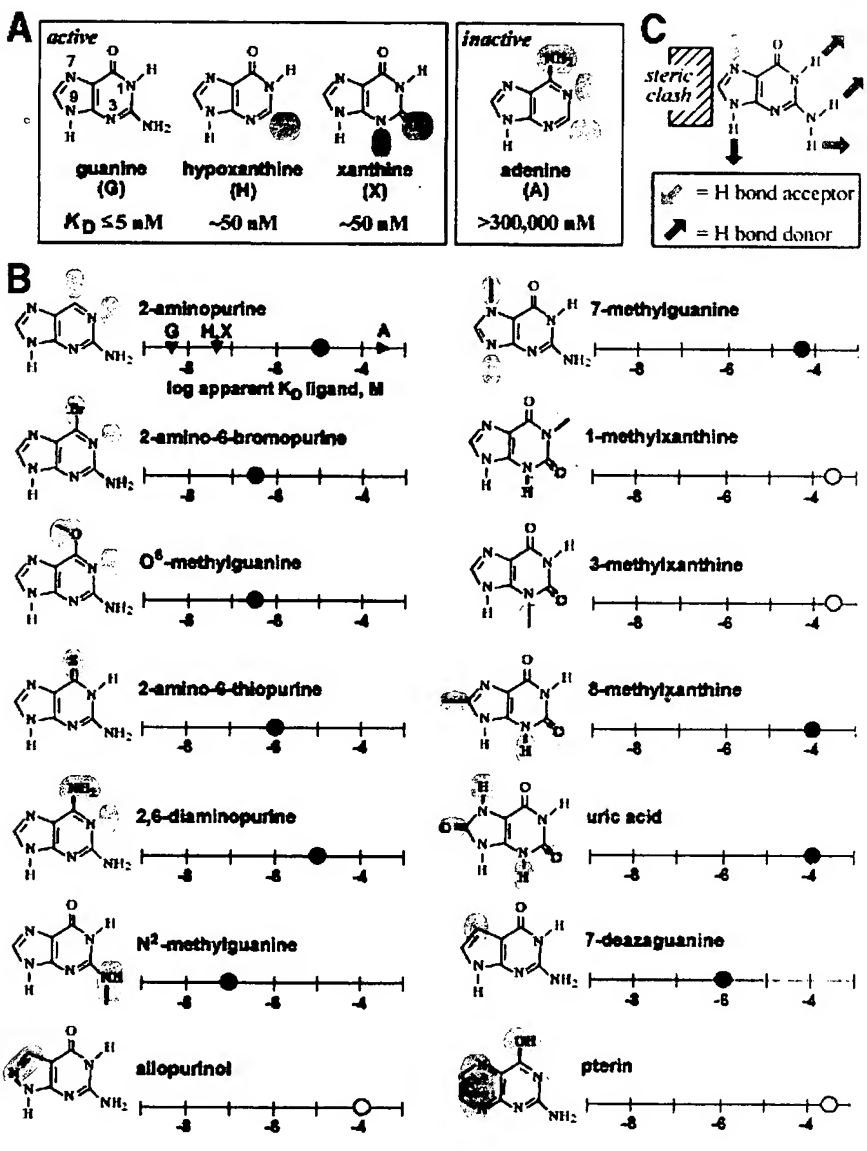

A
active
guanine (G)
hypoxanthine (H)
xanthine (X)
$K_D \leq 5$ nM
~50 nM
~50 nM
inactive
adenine (A)
>300,000 nM
C
steric clash
= H bond acceptor
= H bond donor
B
2-aminopurine
G H X A
-8 -6 -4
log apparent K_D ligand, M
2-amino-6-bromopurine
O^6-methylguanine
2-amino-6-thiopurine
2,6-diaminopurine
N^2-methylguanine
allopurinol
7-methylguanine
1-methylxanthine
3-methylxanthine
8-methylxanthine
uric acid
7-deazaguanine
pterin

FIG 26

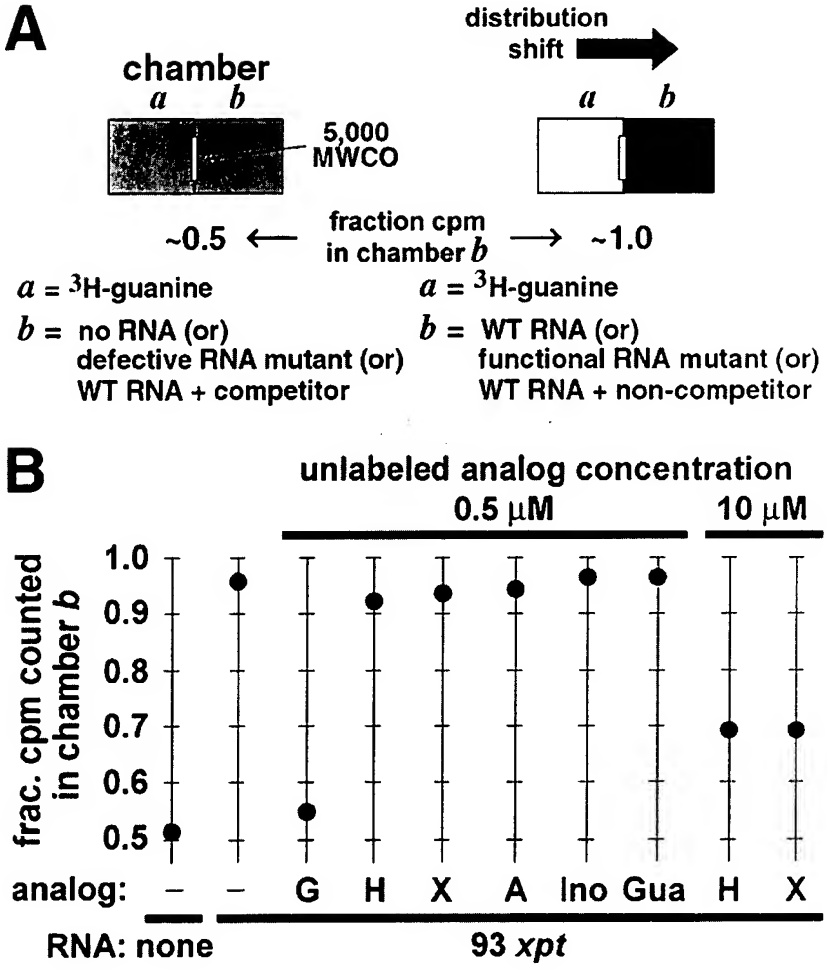

A
chamber
a
b
5,000 MWCO
distribution shift
a
b
~0.5
fraction cpm in chamber b
~1.0
a = 3H-guanine
b = no RNA (or) defective RNA mutant (or) WT RNA + competitor
a = 3H-guanine
b = WT RNA (or) functional RNA mutant (or) WT RNA + non-competitor
B
unlabeled analog concentration
0.5 μM
10 μM
frac. cpm counted in chamber b
1.0
0.9
0.8
0.7
0.6
0.5
analog: – – G H X A Ino Gua H X
RNA: none
93 xpt

FIG 27

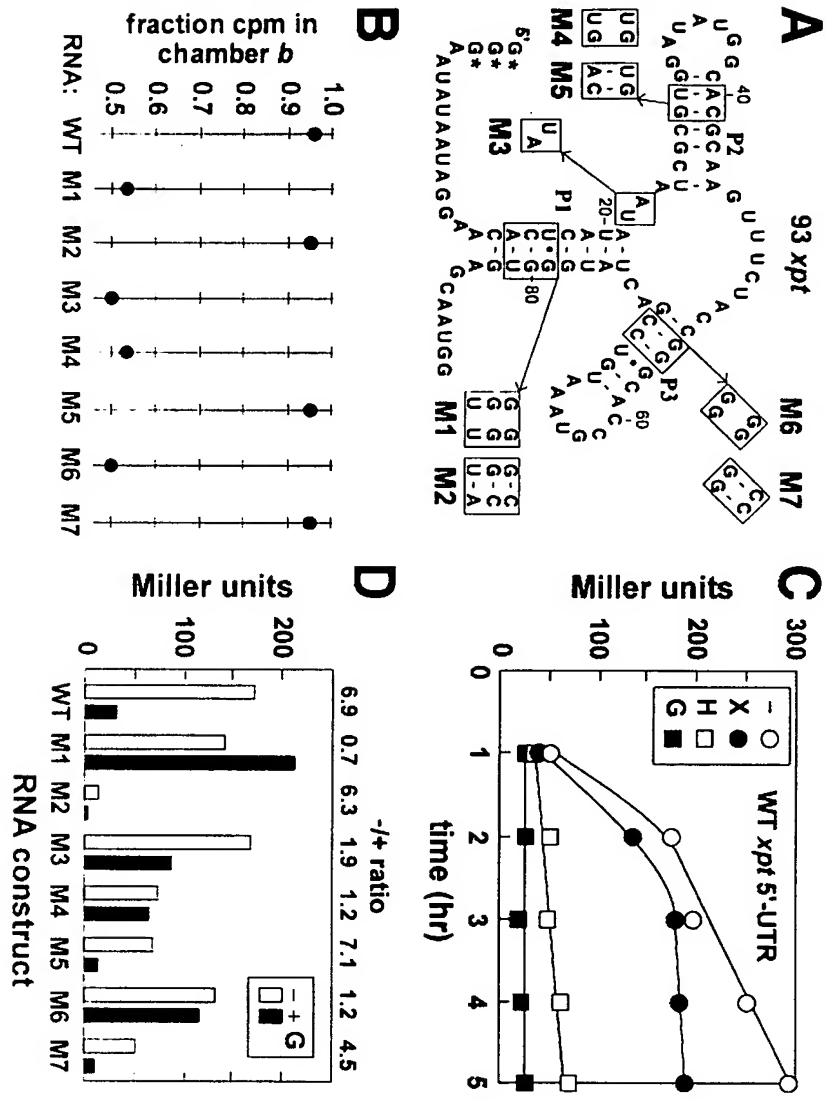
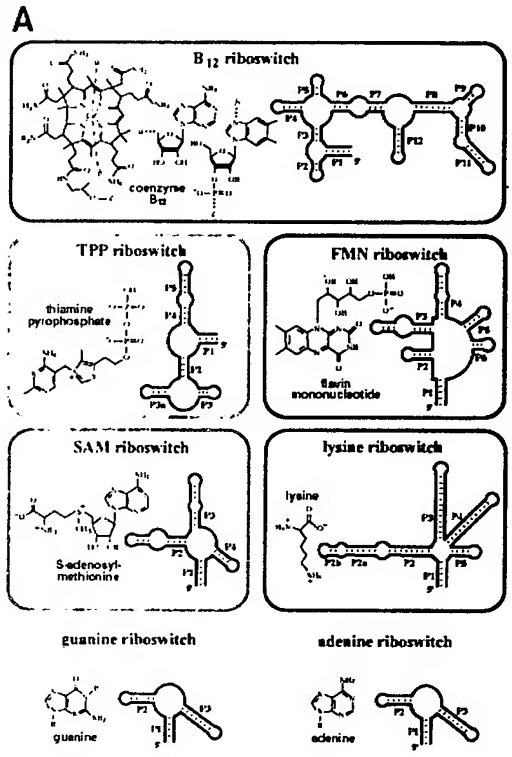

A
93 xpt
M4 M5
M3
M6 M7
M1 M2
P1
P2
P3
B
fraction cpm in chamber b
RNA: WT M1 M2 M3 M4 M5 M6 M7
C
Miller units
time (hr)
WT xpt 5'-UTR
X H G
D
Miller units
-/+ ratio
6.9 0.7 6.3 1.9 1.2 7.1 1.2 4.5
RNA construct
WT M1 M2 M3 M4 M5 M6 M7
- + G

FIG. 28


A
B12 riboswitch
coenzyme B12
TPP riboswitch
thiamine pyrophosphate
FMN riboswitch
flavin mononucleotide
SAM riboswitch
S-adenosyl-methionine
lysine riboswitch
lysine
guanine riboswitch
guanine
adenine riboswitch
adenine

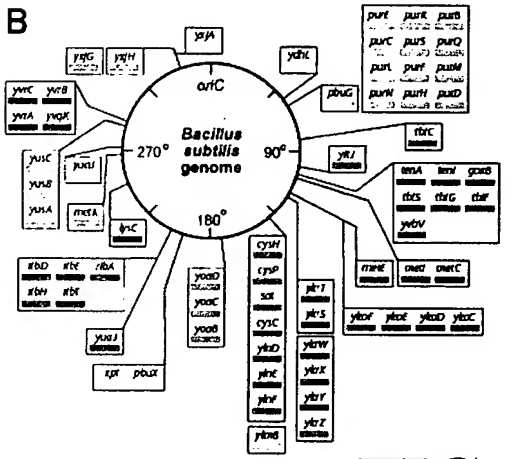

B
Bacillus subtilis genome
0°
90°
180°
270°

FIG. 29

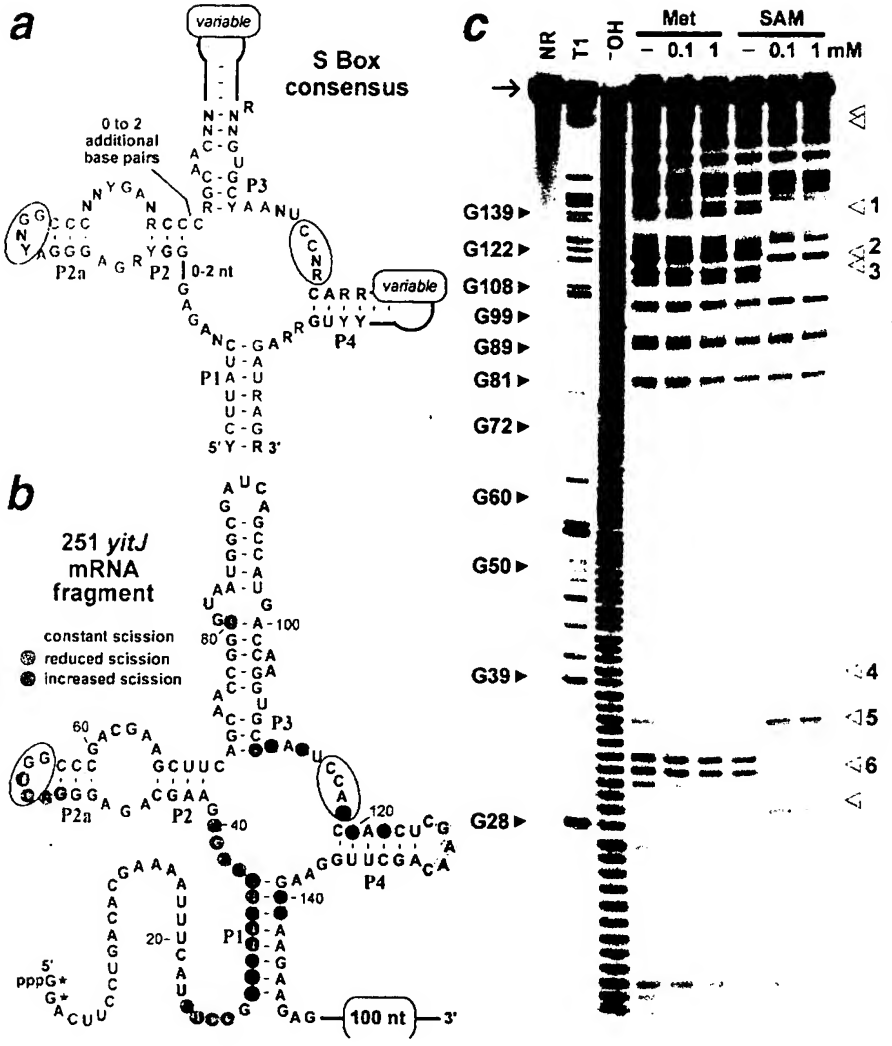

a
variable
S Box consensus
0 to 2 additional base pairs
P3
P2a
P2
0-2 nt
P1
P4
variable
5' Y - R 3'
b
251 yitJ mRNA fragment
constant scission
reduced scission
increased scission
100 nt
3'
c
NR
T1
-OH
Met
SAM
– 0.1 1
– 0.1 1 mM
G139
G122
G108
G99
G89
G81
G72
G60
G50
G39
G28
1
2
3
4
5
6

FIG. 30

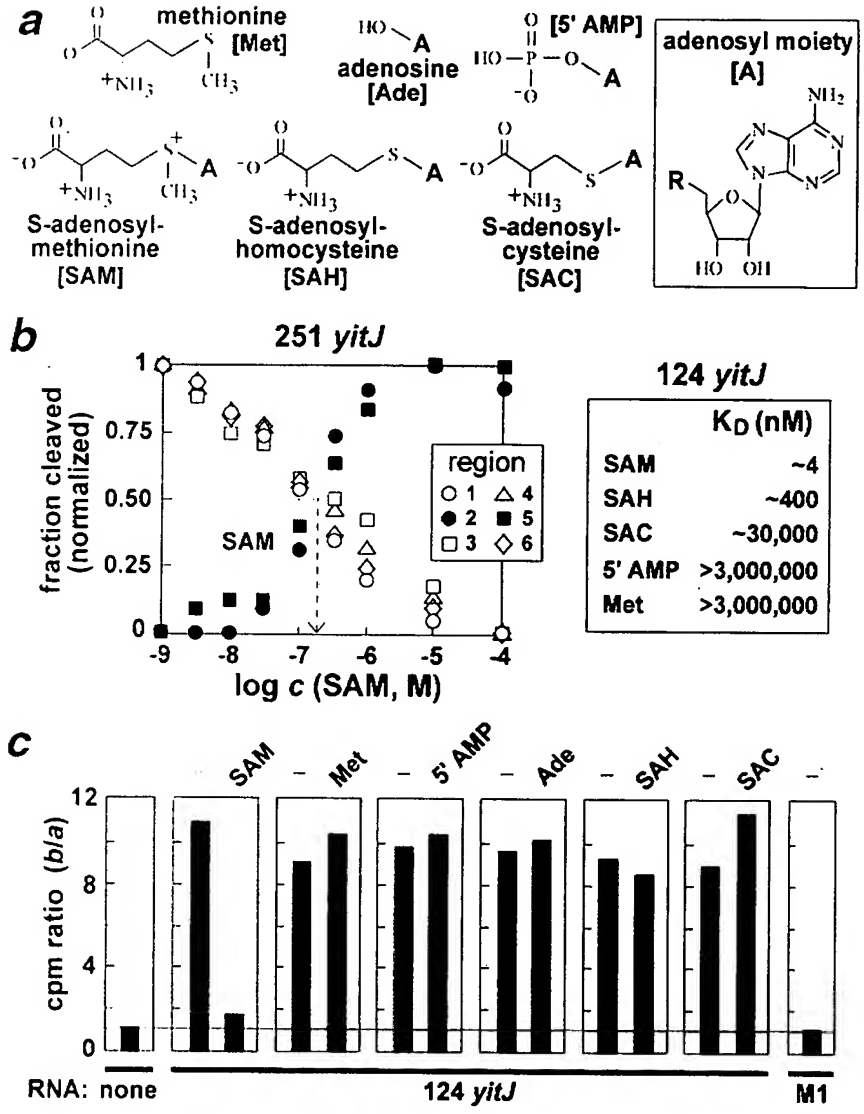

a
methionine [Met]
adenosine [Ade]
[5' AMP]
adenosyl moiety [A]
S-adenosyl-methionine [SAM]
S-adenosyl-homocysteine [SAH]
S-adenosyl-cysteine [SAC]
b
251 yitJ
fraction cleaved (normalized)
log c (SAM, M)
region
SAM
124 yitJ
KD (nM)
SAM ~4
SAH ~400
SAC ~30,000
5' AMP >3,000,000
Met >3,000,000
c
SAM
Met
5' AMP
Ade
SAH
SAC
cpm ratio (b/a)
RNA: none
124 yitJ
M1

FIG. 31

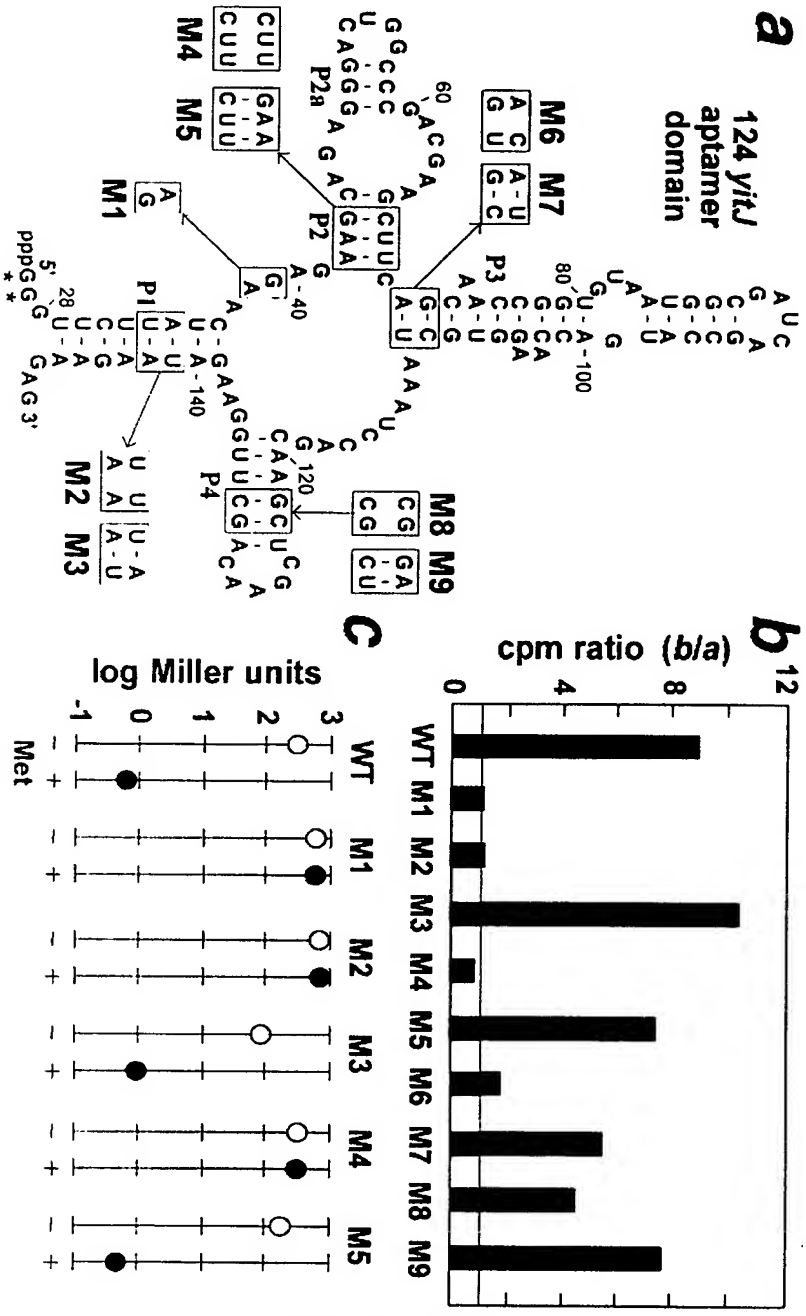

a
124 yitJ aptamer domain
M1
M2
M3
M4
M5
M6
M7
M8
M9
P1
P2
P2a
P3
P4
b
cpm ratio (b/a)
WT M1 M2 M3 M4 M5 M6 M7 M8 M9
c
log Miller units
Met
WT
M1
M2
M3
M4
M5

FIG. 32

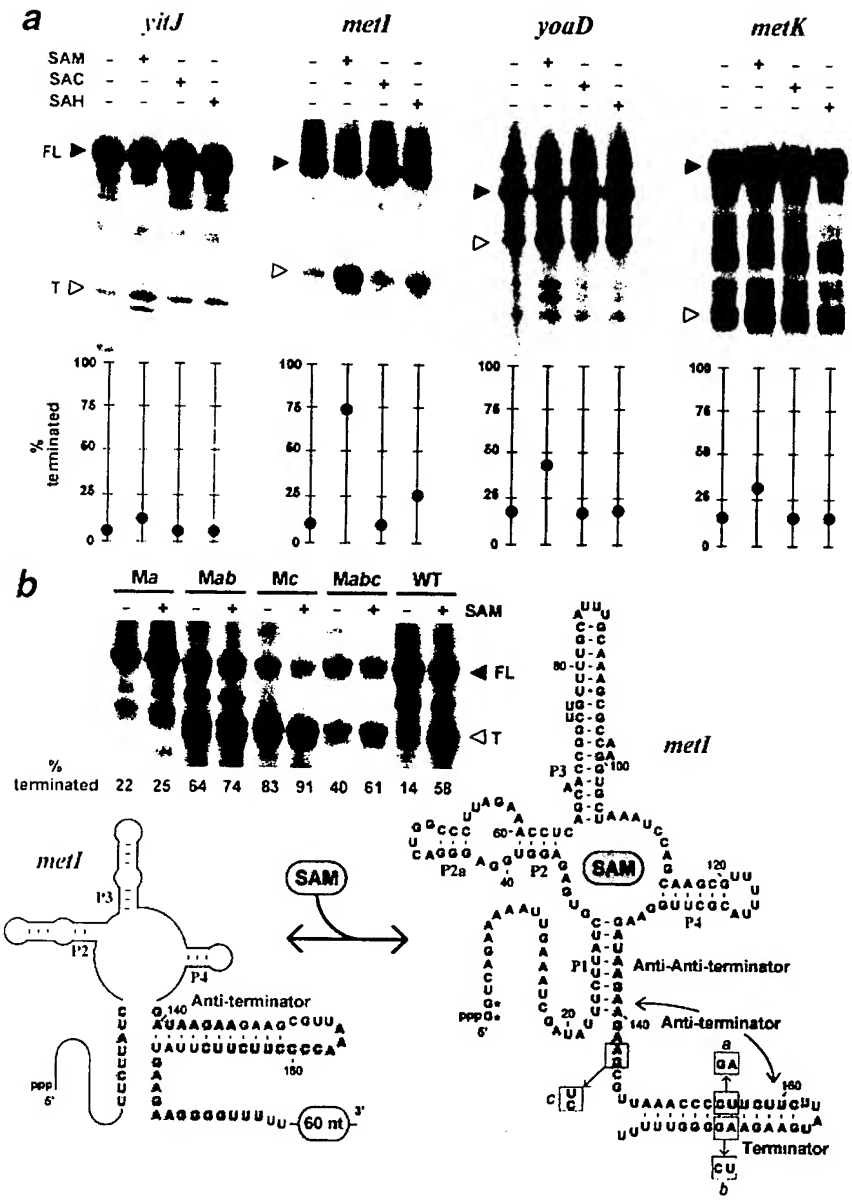

a
yitJ
metI
yoaD
metK
SAM
SAC
SAH
FL
T
% terminated
b
Ma
Mab
Mc
Mabc
WT
% terminated 22 25 64 74 83 91 40 61 14 58
metI
Anti-terminator
60 nt
SAM
Anti-Anti-terminator
Terminator

FIG. 33

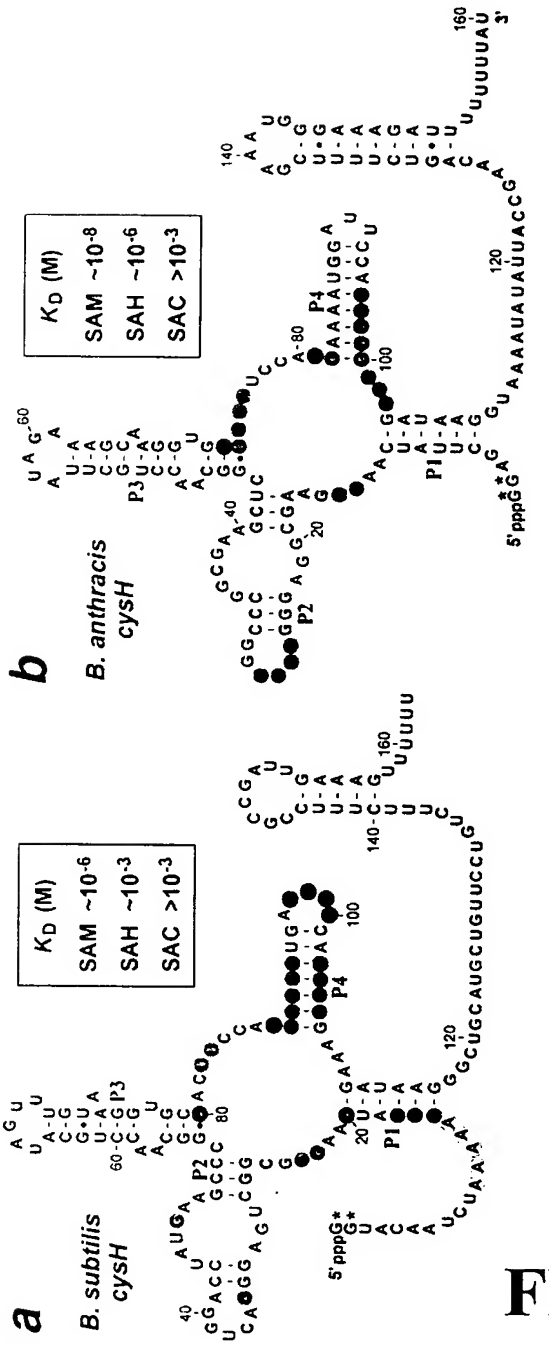

a
B. subtilis
cysH
K_D (M)
SAM ~10-6
SAH ~10-3
SAC >10-3
b
B. anthracis
cysH
K_D (M)
SAM ~10-8
SAH ~10-6
SAC >10-3

FIG. 34

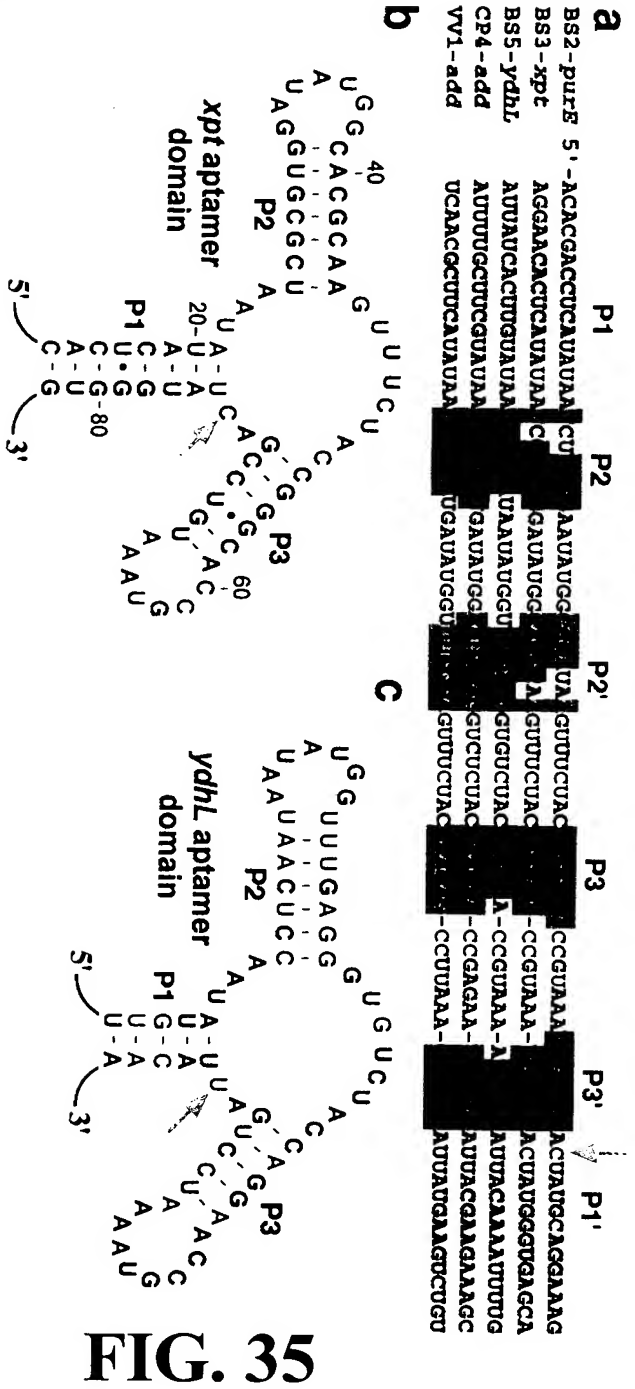

a
BS2-purE
BS3-xpt
BS5-ydhL
CP4-add
VV1-add
P1
P2
P2'
P3
P3'
P1'
b
xpt aptamer domain
P1
P2
P3
c
ydhL aptamer domain
P1
P2
P3

FIG. 35

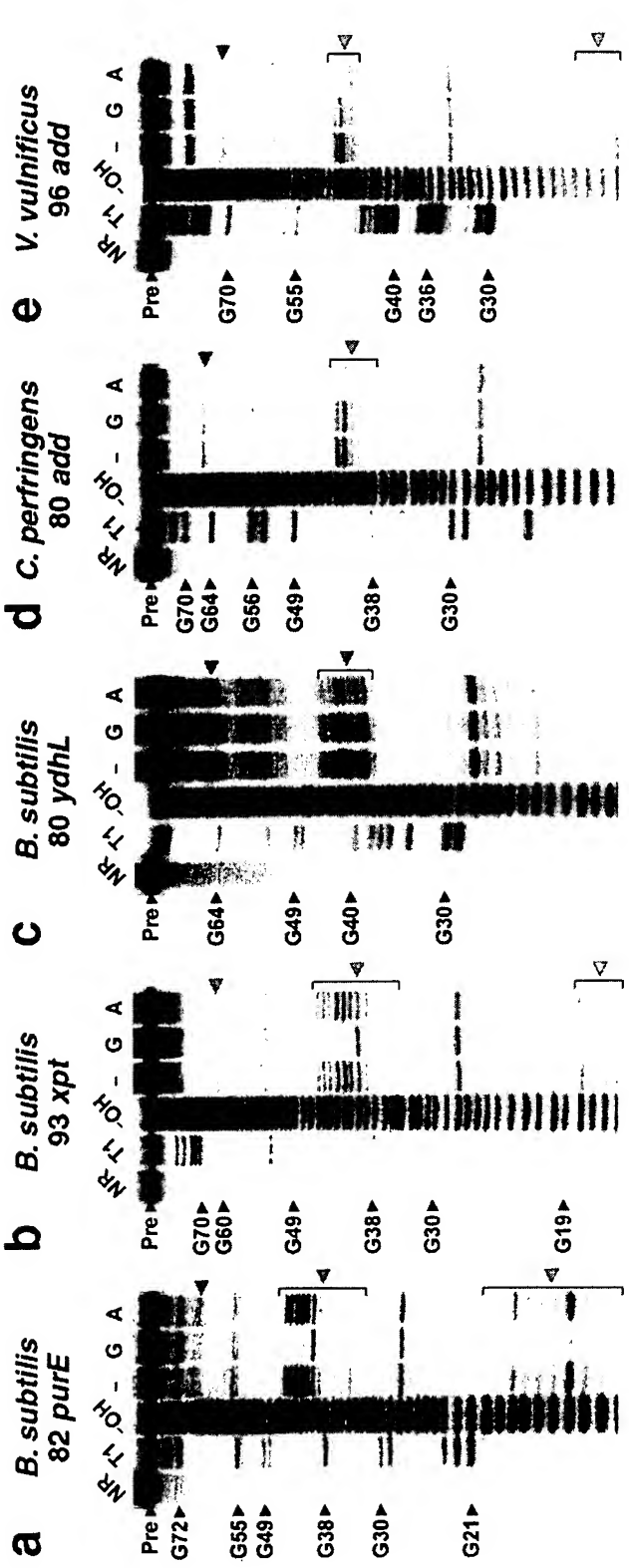

a
B. subtilis
82 pureE
Pre
G72
G55
G49
G38
G30
G21
b
B. subtilis
93 xpt
Pre
G70
G60
G49
G38
G30
G19
c
B. subtilis
80 ydhL
Pre
G64
G49
G40
G30
d
C. perfringens
80 add
Pre
G70
G64
G56
G49
G38
G30
e
V. vulnificus
96 add
Pre
G70
G55
G40
G36
G30
NR
OH
T1
G
A

FIG 36

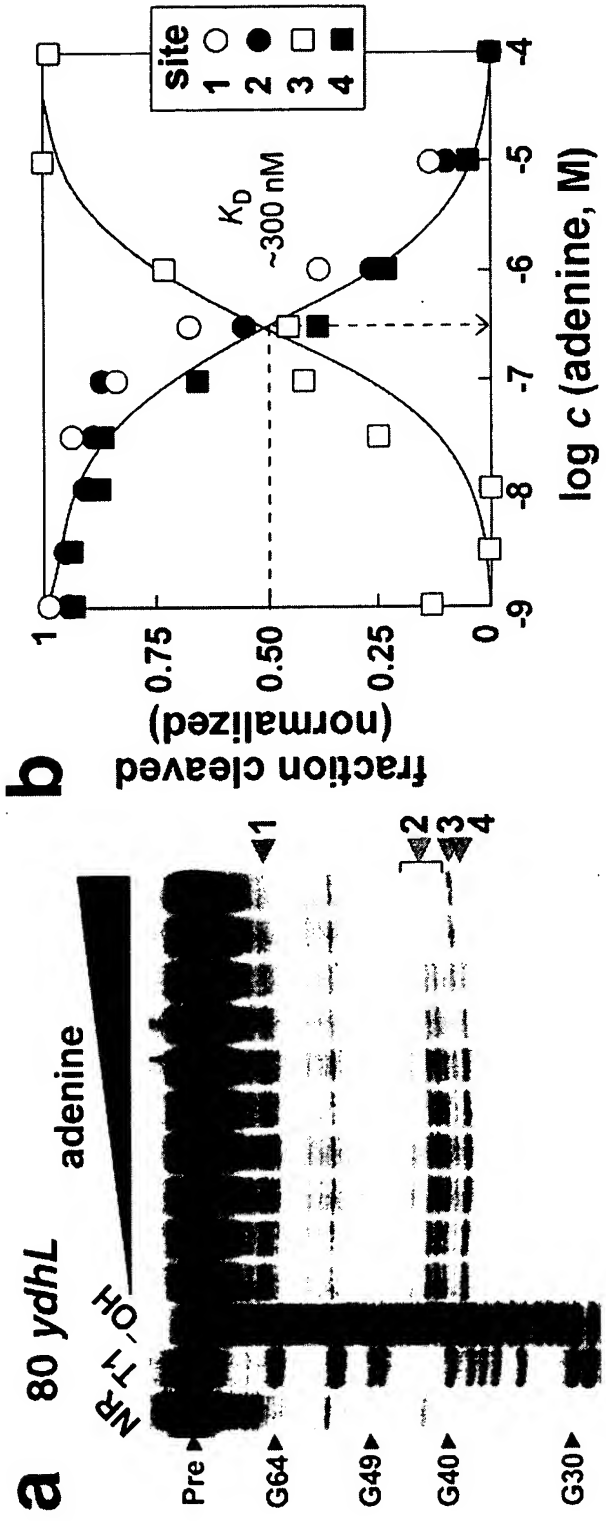

b
fraction cleaved (normalized)
1
0.75
0.50
0.25
0
site
1
2
3
4
K_D ~300 nM
-4
-5
-6
-7
-8
-9
log c (adenine, M)
a
80 ydhL
adenine
NR_1.7_OH
1
2
3
4
Pre
G64
G49
G40
G30

FIG 37

a
2,6-diaminopurine (2,6-DAP)
adenine (A)
2-aminopurine (2-AP)
guanine (G)
purine (P)
N6-methyladenine (MA)
KD ~10 nM
~300 nM
~300 nM
>10,000 nM
~30,000 nM
~100,000 nM
log apparent KD ligand, M
-8
-6
-4
2,6-DAP
A, 2-AP
G
P
MA
other analogs
steric clash
acceptor
donor
b
8-chloro-adenine
1-methyl-adenine
3-methyl-adenine
2-chloro-adenine
8-aza-adenine
N6, N6-methyl-adenine
1-deazapurine
6-cyanopurine
6-mercaptopurine
hypoxanthine
xanthine

FIG. 38

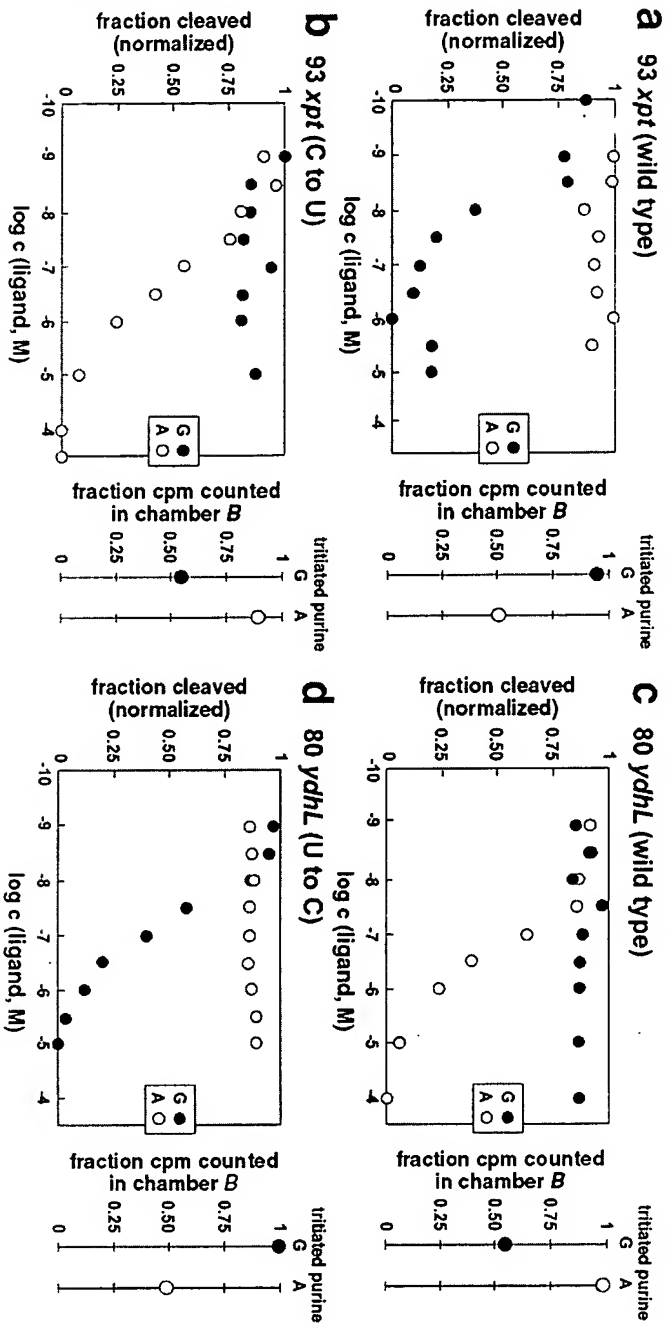

a
93 xpt (wild type)
b
93 xpt (C to U)
c
80 ydhL (wild type)
d
80 ydhL (U to C)
fraction cleaved (normalized)
log c (ligand, M)
fraction cpm counted in chamber B
tritiated purine
G
A

FIG. 39

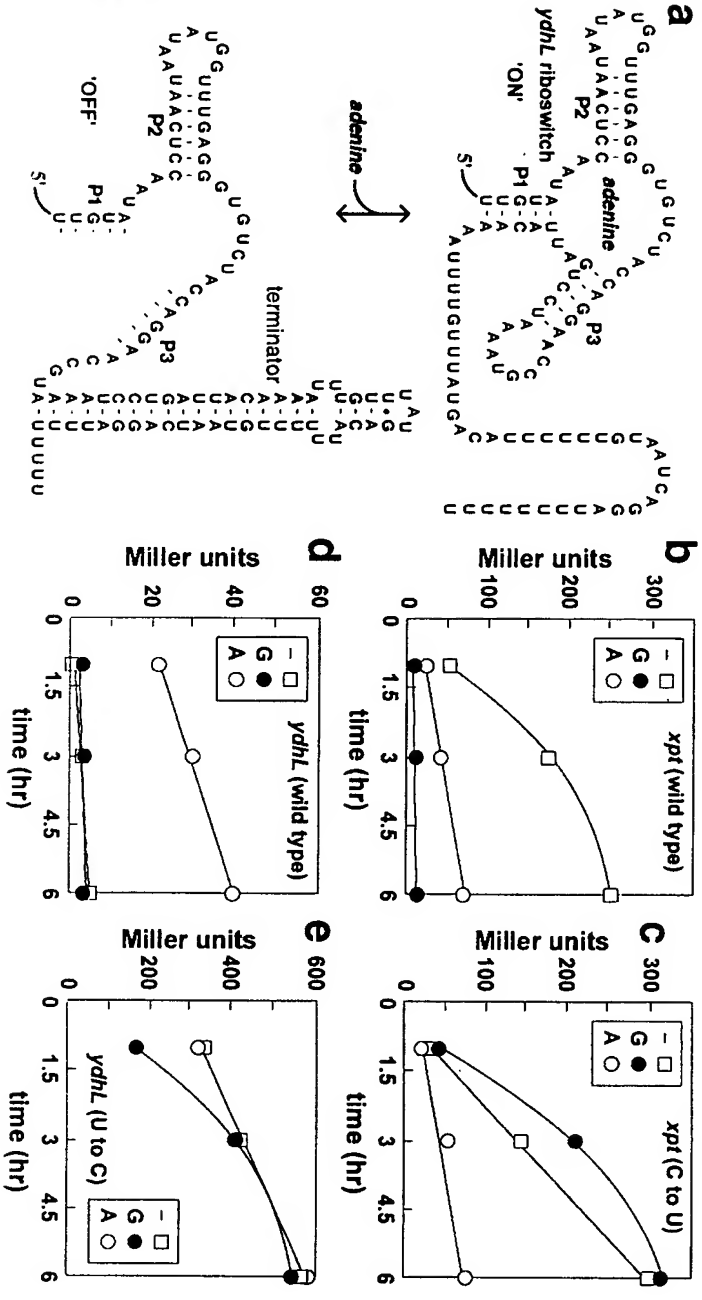

a
ydhL riboswitch
'ON'
'OFF'
adenine
terminator
P1
P2
P3
5'
b
xpt (wild type)
c
xpt (C to U)
d
ydhL (wild type)
e
ydhL (U to C)
Miller units
time (hr)
G
A
–

FIG. 40

Figure 41

A. Alignment of SAM Riboswitches.

Table S1. S Box Sequence Alignment

ID	Position	Genbank Acc.	Organism	Remark	Start	Operon	
Bs01	-	1180274	NC_000964.1 Bacillus subtilis		92	metF	(yitJ)
Bs02	+	1257777	NC_000964.1 Bacillus subtilis		70	metB-metC	(yjcI)
Bs03	-	1385353	NC_000964.1 Bacillus subtilis		130	metE	(metC)
Bs04	-	1424147	NC_000964.1 Bacillus subtilis	(*)	89	ykrT-GCN3	(ykrT)
Bs05	+	1426344	NC_000964.1 Bacillus subtilis		60	rbcL-ykrX-araD-ykrZ	(ykrW)
Bs06	+	1629516	NC_000964.1 Bacillus subtilis		164	cysH-pitA-MET3-cysC	(cysH)
Bs07	-	2024504	NC_000964.1 Bacillus subtilis		86	ldhA-xylB	(yoaD)
Bs08	-	3128412	NC_000964.1 Bacillus subtilis		170	metK	(metE)
Bs09	-	3363560	NC_000964.1 Bacillus subtilis		108	abc -2011-nlpA	(yusC)
Bs10	+	3996569	NC_000964.1 Bacillus subtilis		85	metE	(yxjH)
Bs11	+	3997959	NC_000964.1 Bacillus subtilis		80	metE	(yxjG)
Bh01	-	910190	NC_002570.1 Bacillus halodurans		141	????	
Bh02	+	1348818	NC_002570.1 Bacillus halodurans		99	thrA	
Bh03	+	1699959	NC_002570.1 Bacillus halodurans		175	metB-metC-metF-metH	

Bh04 - 3427466 NC_002570.1 Bacillus halodurans			157 metK
Bh05 - 3591166 NC_002570.1 Bacillus halodurans			220 abc -2011-nlpA
Oi01 + 727028 NC_004193.1 Oceanobacillus iheyensis			78 metH
Oi02 - 1098097 NC_004193.1 Oceanobacillus iheyensis			162 metE
Oi03 + 1319043 NC_004193.1 Oceanobacillus iheyensis		(1)	76 ????
Oi04 - 2134364 NC_004193.1 Oceanobacillus iheyensis			56 abc -????-nlpA
Oi05 - 2365511 NC_004193.1 Oceanobacillus iheyensis			176 metK
Oi06 - 2437305 NC_004193.1 Oceanobacillus iheyensis			129 abc -????-nlpA
Oi07 - 2708643 NC_004193.1 Oceanobacillus iheyensis			177 tran-MET17
Oi10 - 3200636 NC_004193.1 Oceanobacillus iheyensis			81 ????-????
Oi08 - 2856863 NC_004193.1 Oceanobacillus iheyensis			201 ????-????
Oi09 + 3162075 NC_004193.1 Oceanobacillus iheyensis			105 MET17
Oi10 - 3200636 NC_004193.1 Oceanobacillus iheyensis			81 ????-????
Oi11 + 3200766 NC_004193.1 Oceanobacillus iheyensis			94 ????
Oi12 + 3294474 NC_004193.1 Oceanobacillus iheyensis			97 abc-2011-nlpA-abgB
Oi13 - 3466518 NC_004193.1 Oceanobacillus iheyensis			112 gldA-nlpA-abc-2011
Ca01 + 453565 NC_003030.1 Clostridium acetobutylicum			78 metB-metC
Ca02 - 671354 NC_003030.1 Clostridium acetobutylicum			77 metH
Ca03 - 1073886 NC_003030.1 Clostridium acetobutylicum		(2)	(smtA-metB-cysK)
Ca04 + 1131539 NC_003030.1 Clostridium acetobutylicum			81 abc-2011-nlpA

Ca05	+	1976373	NC_003030.1	Clostridium acetobutylicum	102 metA
Ca06	-	2914839	NC_003030.1	Clostridium acetobutylicum	117 CAC5
Ca07	-	2991405	NC_003030.1	Clostridium acetobutylicum	70 metK
Cp01	-	2500081	NC_003366.1	Clostridium perfringens	391 metK
Cp02	-	2665229	NC_003366.1	Clostridium perfringens	102 nhaC
Lm01	+	137135	NC_003210.1	Listeria monocytogenes	90 oppA-dppB-dppC
Lm02	-	309383	NC_003210.1	Listeria monocytogenes	113 nlpA-abc-2011
Lm03	-	637924	NC_003210.1	Listeria monocytogenes	111 MET17-MET2
Lm04	+	882772	NC_003210.1	Listeria monocytogenes	97 metE
Lm05	-	1716649	NC_003210.1	Listeria monocytogenes	110 metK
Lm06	-	1739595	NC_003210.1	Listeria monocytogenes	109 metE-metB-metC-metH
Lm07	-	2491174	NC_003210.1	Listeria monocytogenes	93 abc-2011-nlpA
Li01	+	172401	NC_003212.1	Listeria innocua (*)	88 oppA-dppB-dppC
Li02	-	327333	NC_003212.1	Listeria innocua (*)	113 nlpA-abc-2011
Li03	-	636911	NC_003212.1	Listeria innocua (*)	111 met17-met2
Li04	+	871751	NC_003212.1	Listeria innocua (*)	97 metE
Li05	-	1772459	NC_003212.1	Listeria innocua (*)	110 metK
Li06	-	1790189	NC_003212.1	Listeria innocua (*)	109 metE-metB-metC-metH
Li07	-	2538251	NC_003212.1	Listeria innocua (*)	92 abc-2011-nlpA
Sa01	+	15958	NC_002745.1	Staphylococcus aureus	41 met2

Sa02	+	875385	NC_002745.1	Staphylococcus aureus	91	abc-2011-nlpA
Sa03	-	1844603	NC_002745.1	Staphylococcus aureus	108	metK
Sa04	-	2381620	NC_002745.1	Staphylococcus aureus	13	nhaC
Sc01	+	4708438	NC_003888.1	Streptomyces coelicolor	26	thrC-moaD

ID	Position	Genbank Acc.	Organism	Remark	Start	Operon
Ct01	+	606192	AE_006470 Chlorobium tepidum		107	CAC5-MET2
Tt01	+	500245	NC_003869.1 Thermoanaerobacter tengcongensis		55	metK
Tt02	-	1750367	NC_003869.1 Thermoanaerobacter tengcongensis		66	metF-metH-ebsC
Tt03	-	2076680	NC_003869.1 Thermoanaerobacter tengcongensis		78	thrA-CAC5
Fn01	-	987483	NC_003454.1 Fusobacterium nucleatum		84	metK
Fn02	-	1317650	NC_003454.1 Fusobacterium nucleatum	(*)	91	abc-2011-nlpA
Dr01	+	1363063	NC_001263.1 Deinococcus radiodurans, chr 1		156	abc-2011-nlpA-nlpA
Dr02	+	980704	NC_001263.1 Deinococcus radiodurans, chr 1		41	metH-????-metF
Xa01	-	3558018	NC_003919.1 Xanthomonas axonopodis		74	MET2-metC-thrA
Xc01	-	3379769	NC_003902.1 Xanthomonas campestris	(*)	73	MET2-metC-thrA
Se01	+	574	AF_269983.1 Staphylococcus epidermidis genomic clone			
Se02	-	142	AF_270301.1 Staphylococcus epidermidis genomic clone			(*)
Gs01	+	342843	contig:2947 Geobacter sulferreducens			
Gs02	+	2470946	contig:2947 Geobacter sulferreducens			
Ba01	-	177272	contig:6615 Bacillus anthracis			
Ba02	+	185586	contig:6615 Bacillus anthracis			
Ba03	-	197185	contig:6615 Bacillus anthracis			
Ba04	+	320607	contig:6615 Bacillus anthracis			

Ba05 - 371127 contig:6615 Bacillus anthracis

Ba06 + 1362659 contig:6615 Bacillus anthracis

Ba07 + 1375353 contig:6615 Bacillus anthracis

Ba08 + 2459362 contig:6615 Bacillus anthracis

Ba09 - 2953226 contig:6615 Bacillus anthracis

Ba10 - 3091676 contig:6615 Bacillus anthracis

Ba11 - 3890736 contig:6615 Bacillus anthracis

Ba12 + 3892933 contig:6615 Bacillus anthracis

Ba13 + 4074285 contig:6615 Bacillus anthracis

Ba14 - 4074078 contig:6615 Bacillus anthracis

Ba15 - 4553682 contig:6615 Bacillus anthracis

Ba16 - 4739975 contig:6615 Bacillus anthracis (*)

Ba17 - 5140322 contig:6615 Bacillus anthracis

Bc01 + 26115 contig:1617 Bacillus cereus (*)

Bc02 + 748841 contig:1617 Bacillus cereus

Bc03 + 1183078 contig:1617 Bacillus cereus (*)

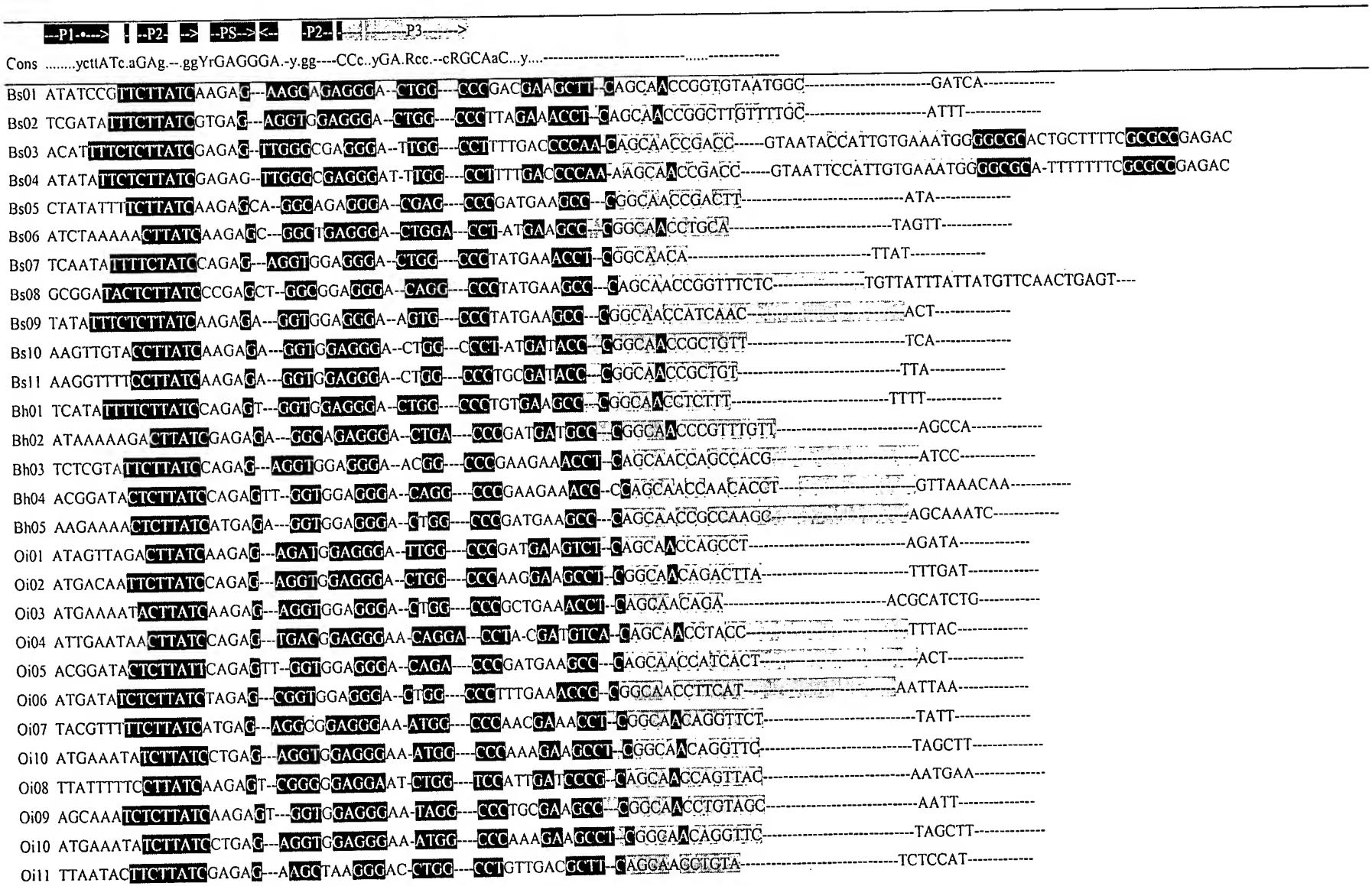
Bc04 + 1195849 contig:1617 Bacillus cereus (*)

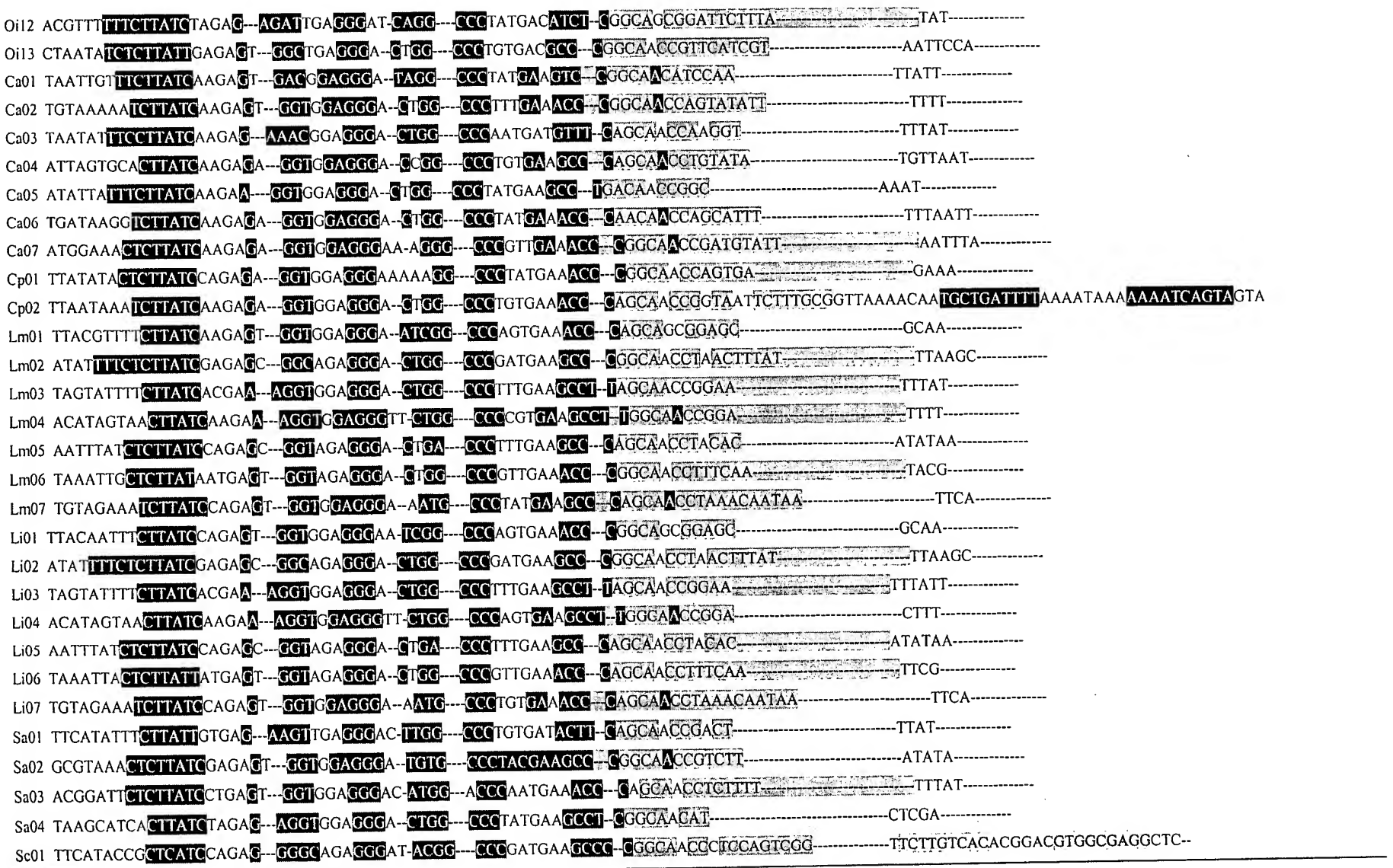
Bc05 + 2200884 contig:1617 Bacillus cereus (*)

Bc06 - 2684484 contig:1617 Bacillus cereus (*)

Bc07 - 2963724 contig:1617 Bacillus cereus

Bc08 - 2773209 contig:1617	Bacillus cereus	(*)
Bc09 + 3500608 contig:1617	Bacillus cereus	(*)
Bc10 - 3687209 contig:1617	Bacillus cereus	(*)
Bc11 + 3687417 contig:1617	Bacillus cereus	(*)
Bc12 - 3498410 contig:1617	Bacillus cereus	(*)
Bc13 - 4205859 contig:1617	Bacillus cereus	(*)
Bc14 - 4397125 contig:1617	Bacillus cereus	(*)
Bc15 - 4784934 contig:1617	Bacillus cereus	(*)
Bc16 - 5114094 contig:1617	Bacillus cereus	(*)
Bc17 - 5094322 contig:1617	Bacillus cereus	(*)
Bc18 + 5101784 contig:1617	Bacillus cereus	(*)


--P1-•--> | --P2- --> --PS--><-- -P2-- P3---->
Cons .....yctlATc.aGAg.--.ggYrGAGGGA.-y.gg----CCc..yGA.Rcc.--cRGCAaC...y....
Bs01 ATATCCGTTCTTATCAAGAG---AAGCAGAGGGA--CTGG----CCGGACGAAGCTT--CAGCAACCGGTGTAATGGC----------GATCA----------
Bs02 TCGATATTTCTTATCGTGAG---AGGTGGAGGGA--CTGG----CCCTTAGAAACCT--CAGCAACCGGCTTGTTTTGC----------ATTT----------
Bs03 ACATTTTCTCTTATCGAGAG--TTGGGCGAGGGA--TTGG----CCTTTTGACCCCAA-CAGCAACCGACC------GTAATACCATTGTGAAATGGGGCGGCACTGCTTTTCGCGCCGAGAC
Bs04 ATATATTCTCTTATCGAGAG--TTGGGCGAGGGAT-TTGG----CCTTTTGACCCCAA-AAGCAACCGACC------GTAATTCCATTGTGAAATGGGGCGGCA-TTTTTTTCGCGCCGAGAC
Bs05 CTATATTTTCTTATCAAGAGCA--GGCAGAGGGA--CGAG----CCCGATGAAGCC---CGGCAACCGACTT----------ATA----------
Bs06 ATCTAAAAACTTATCAAGAGC---GGCTGAGGGA--CTGGA---CCT-ATGAAGCG--CGGCAACCTGCA----------TAGTT----------
Bs07 TCAATATTTTCTATCCAGAG---AGGTGGAGGGA--CTGG----CCCTATGAAACCT--CGGCAACA----------TTAT----------
Bs08 GCGGATACTCTTATCCCGAGCT--GGCGGAGGGA--CAGG----CCCTATGAAGCC---CAGCAACCGGTTTCTC----------TGTTATTTATTATGTTCAACTGAGT----
Bs09 TATATTTCTCTTATCAAGAGA---GGTGGAGGGA--AGTG----CCCTATGAAGCC---CGGCAACCATCAAC----------ACT----------
Bs10 AAGTTGTACCTTATCAAGAGA---GGTGGAGGGA--CTGG---CCCT-ATGATACG---CGGCAACCGCTGTT----------TCA----------
Bs11 AAGGTTTTCCTTATCAAGAGA---GGTGGAGGGA--CTGG----CCCTGCGATACC---CGGCAACCGCTGT----------TTA----------
Bh01 TCATATTTTCTTATCCAGAGT---GGTGGAGGGA--CTGG----CCCTGTGAAGCC---CGGCAACCTCTTT----------TTTT----------
Bh02 ATAAAAAGACTTATCGAGAGA---GGCAGAGGGA--CTGA----CCCGATGATGCC---CGGCAACCCGTTTGTT----------AGCCA----------
Bh03 TCTCGTATTCTTATCCAGAG---AGGTGGAGGGA--ACGG----CCCGAAGAAACCT--CAGCAACCAGCCACG----------ATCC----------
Bh04 ACGGATACTCTTATCCAGAGTT--GGTGGAGGGA--CAGG----CCCGAAGAAACC--CCAGCAACCAACACCT----------GTTAAACAA----------
Bh05 AAGAAAACTCTTATCATGAGA---GGTGGAGGGA--CTGG----CCCGATGAAGCC---CAGCAACCGCCAAGC----------AGCAAATC----------
Oi01 ATAGTTAGACTTATCAAGAG---AGATGGAGGGA--TTGG----CCCGATGAAGTCT--CAGCAACCAGCCT----------AGATA----------
Oi02 ATGACAATTCTTATCCAGAG---AGGTGGAGGGA--CTGG----CCCAAGGAAGCCT--CGGCAACAGACTTA----------TTTGAT----------
Oi03 ATGAAAATACTTATCAAGAG---AGGTGGAGGGA--CTGG----CCCGCTGAAACCT--CAGCAACAGA----------ACGCATCTG----------
Oi04 ATTGAATAACTTATCCAGAG---TGACGGAGGGAA-CAGGA---CCTA-CGATGTCA--CAGCAACCTACC----------TTTAC----------
Oi05 ACGGATACTCTTATTCAGAGTT--GGTGGAGGGA--CAGA----CCCGATGAAGCC---CAGCAACCATCACT----------ACT----------
Oi06 ATGATATCTCTTATCTAGAG---CGGTGGAGGGA--CTGG----CCCTTTGAAACCG--CGGCAACCTTCAT----------AATTAA----------
Oi07 TACGTTTTTCTTATCATGAG---AGGCGGAGGGAA-ATGG----CCCAACGAAACCT--CGGCAACAGGTTCT----------TATT----------
Oi10 ATGAAATATCTTATCCTGAG---AGGTGGAGGGAA-ATGG----CCCAAAGAAGCCT--CGGCAACAGGTTC----------TAGCTT----------
Oi08 TTATTTTTCCTTATCAAGAGT--CGGGGGAGGAAT-CTGG----TCCATTGATCCCG--CAGCAACCAGTTAC----------AATGAA----------
Oi09 AGCAAATCTCTTATCAAGAGT---GGTGGAGGGAA-TAGG----CCCTGCGAAGCC---CGGCAACCTGTAGC----------AATT----------
Oi10 ATGAAATATCTTATCCTGAG---AGGTGGAGGGAA-ATGG----CCCAAAGAAGCCT--CGGGAACAGGTTC----------TAGCTT----------
Oi11 TTAATACTTCTTATCGAGAG---AAGCTAAGGGAC-CTGG----CCTGTTGACGCTT--CAGGAAGGTGTA----------TCTCCAT----------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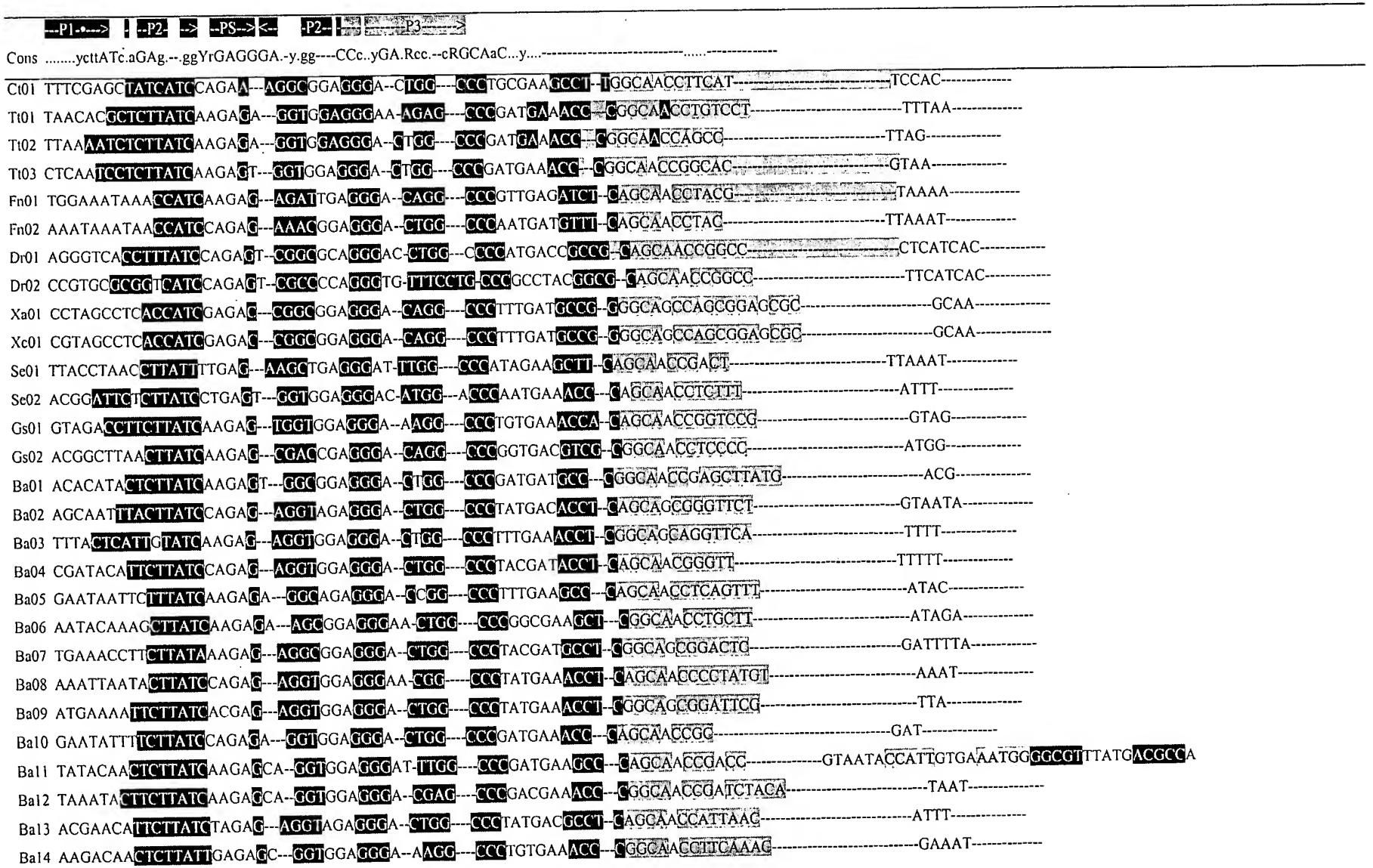
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P2
P2
PS
P2
P3
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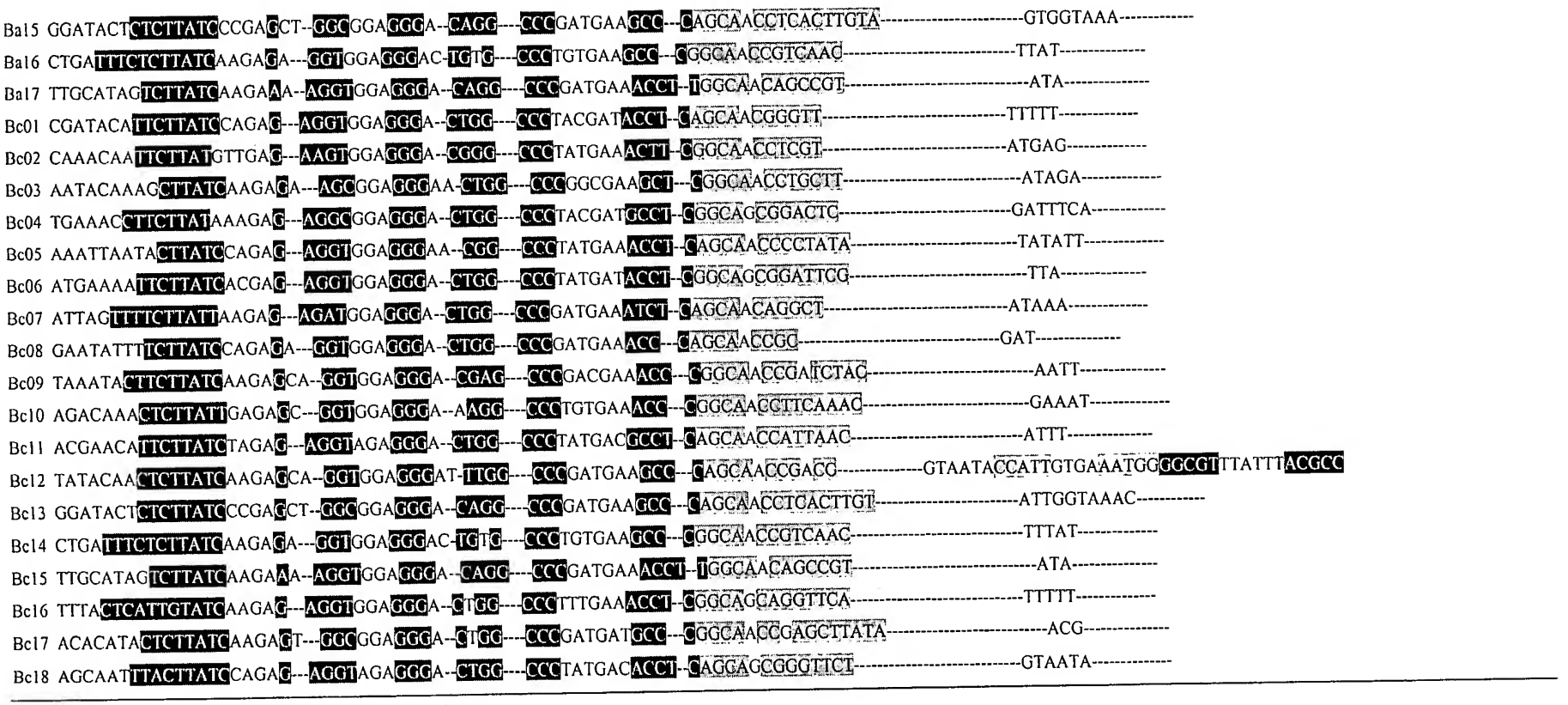
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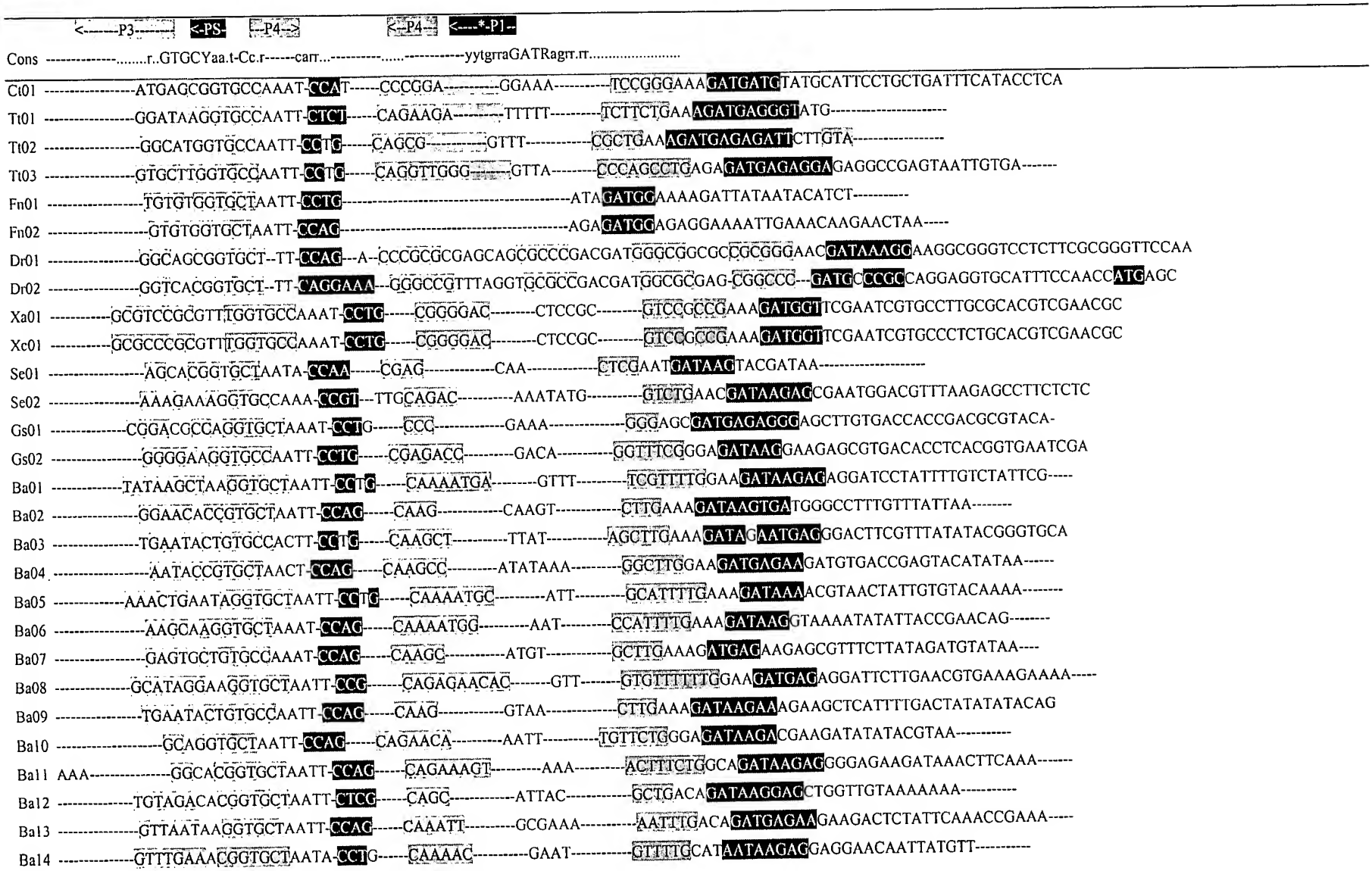
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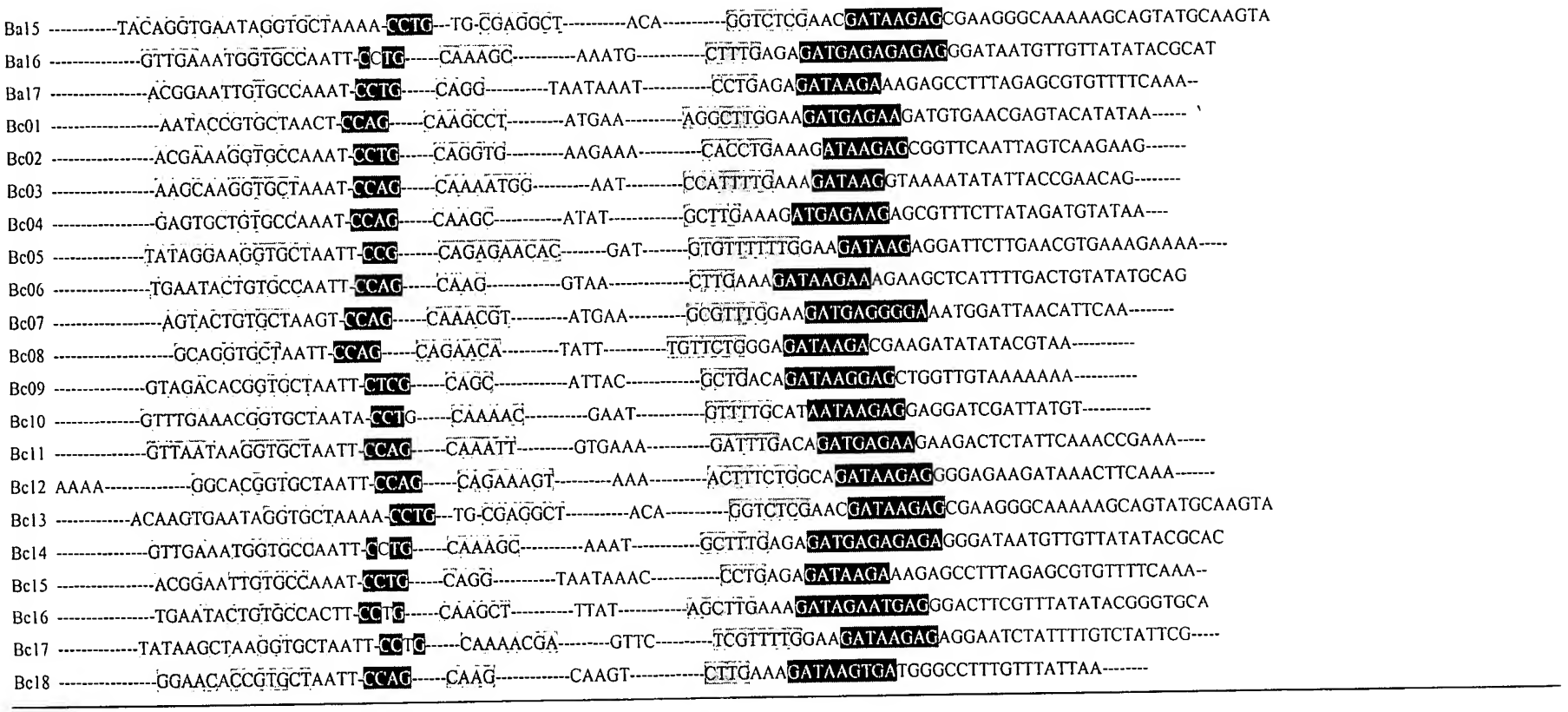
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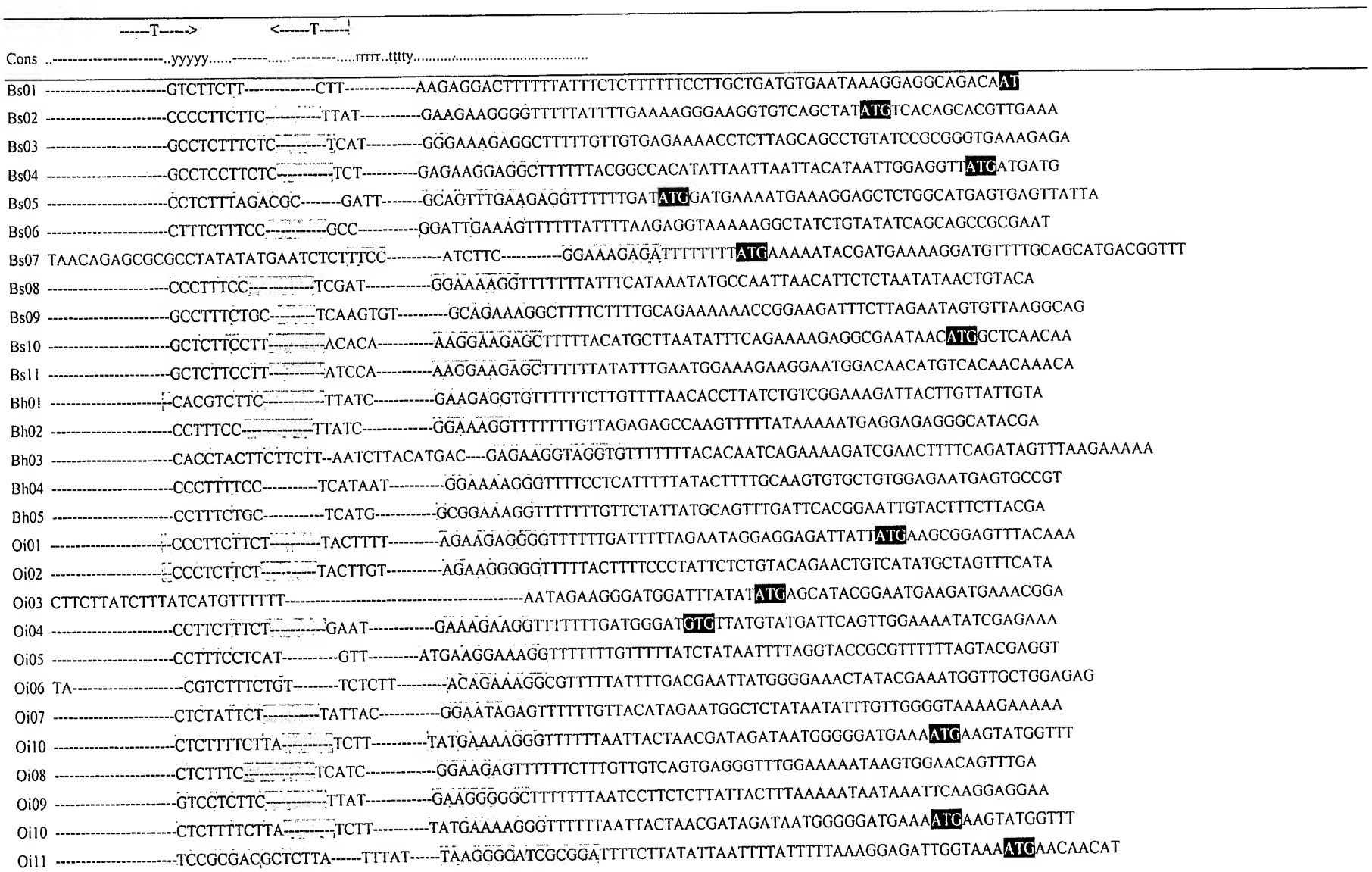
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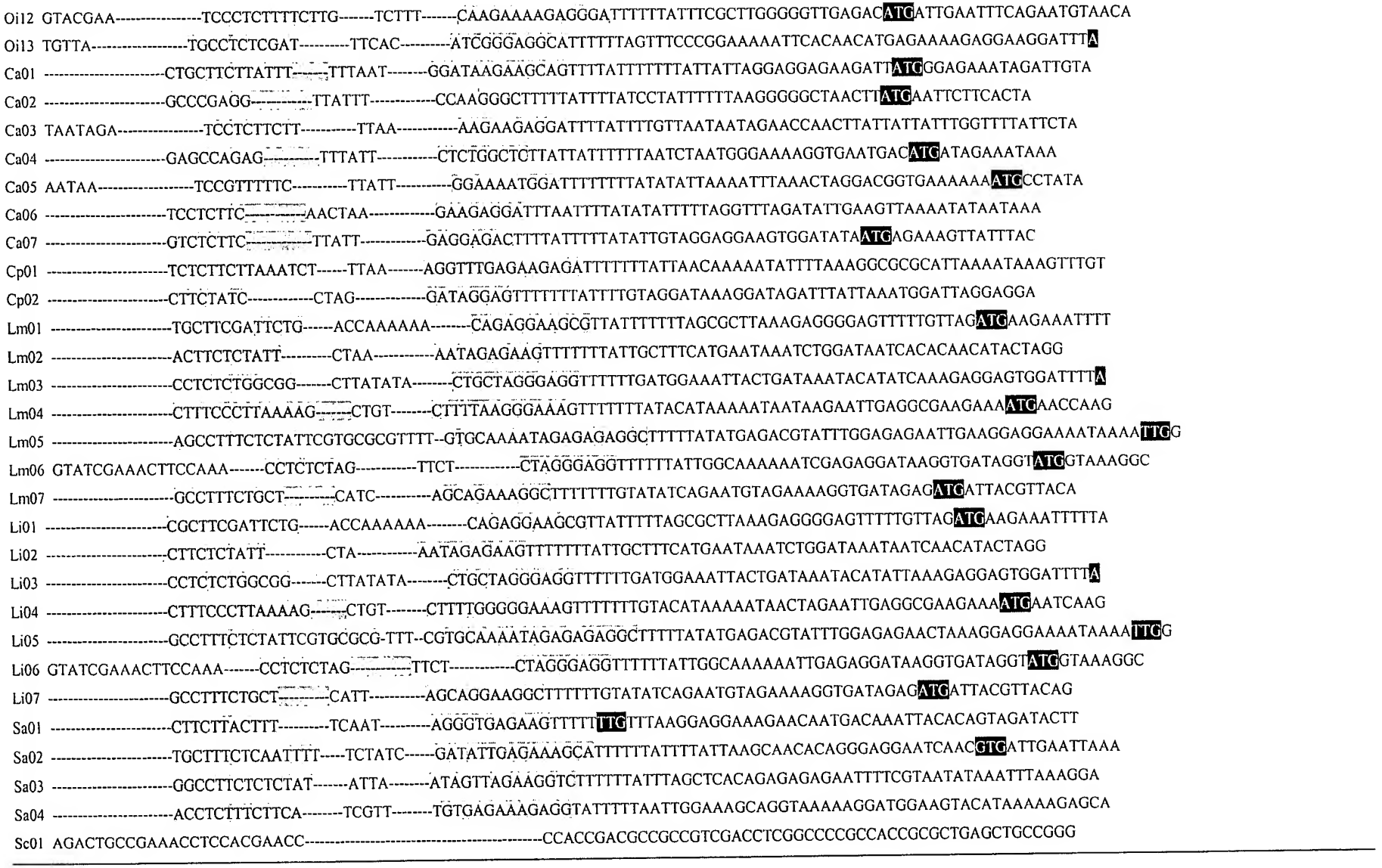
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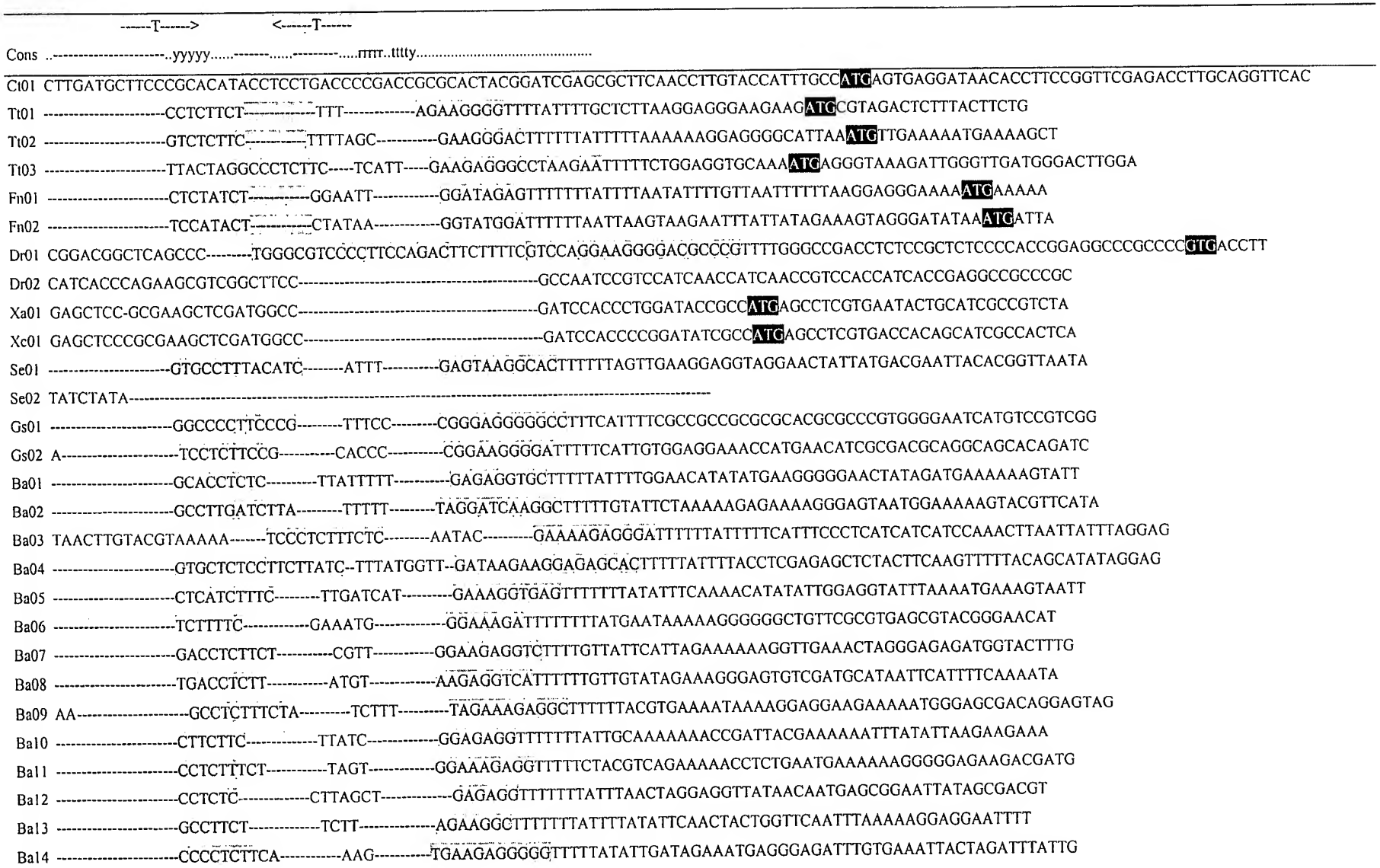
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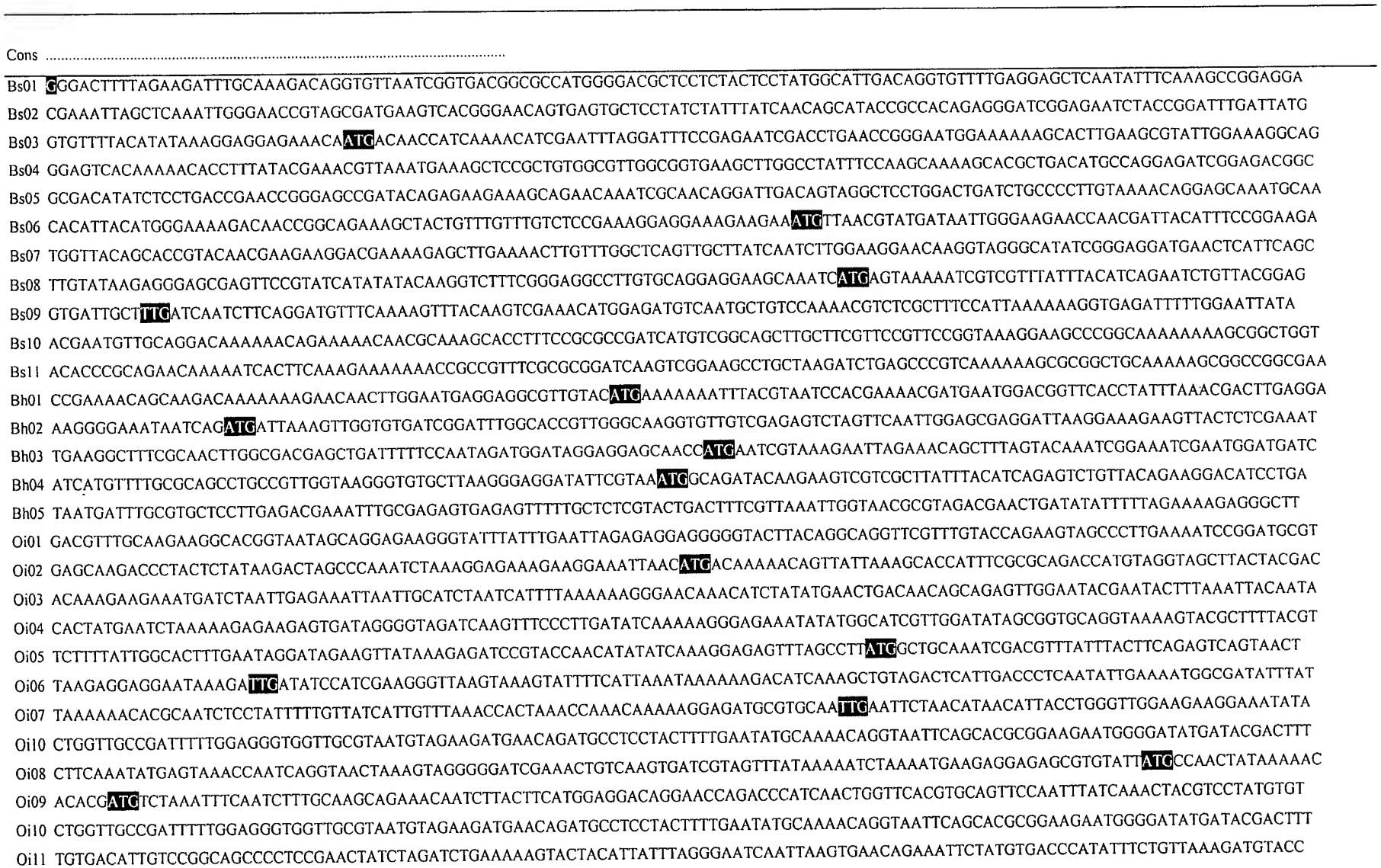
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Ca05 AAAATACCTGATAATCTTCCAGCAGCAAAAACTTTAAATGAAGAAAATATATTTTTTATGGATGAGGATAGAGCCTATCATCAAGATATAAGACCTCTTAATATTGTTATAGTTAACCTT
Ca06 AAGGGGATTTTAAAAATGAGTGAAGAAAGAAAATTTGGTTTTGAAACATTACAGGTTCATGCAGGACAAGTTGCTGATCCAACTACAGGATCAAGAGCTGTACCTATTTATCAAACAACA
Ca07 ATCTGAATCAGTAACAGAAGGGCATCCAGATAAAATCTGCGATCAAATATCAGACGCTATTTTAGATGCCATATTGGAAAAAGATCCAAATGGAAGAGTTGCTTGTGAAACTACAGTGAC
Cp01 TAATTAAGCTTTAAAGATATTATTTTGAATCGTGGGAAGATAAATTAAGTTATTTGTTTAAATAAACAGGGTTGGAATAAATAAAAATGAAAGGGGTGAATTAGCTATCTTATTATGATA
Cp02 GAGAAAATGAAAAAAGGAAAGTTTTCAGCATTATTACCATTAATAATTTTTGTATCGATTTATTTGGGAACTTCATTAGTAATGAAAGATTTCTACTCTGTATCTGTTTTAGTTCCAGGA
Lm01 TATTAGTAGCGGTTATCTCGGTTTTTGCCTTGGTGTTAACGGCTTGCGGAGGTTCTGGCGCTAGTTCAGACAAAGCAAACGGTTCAGGCAAAGCGAAAGACGGCGGCTCTCTTATTATCG
Lm02 GAGGAAAAAAGATGAAAAAATTAACAAAAGGGTTAGGAATTTTACTTGCATCAAGCCTTGTTTTAGGATTAGCAGCATGTGGAGGAGGCAGTGACGATAAAGCCTTAAGCACAGAAAAAA
Lm03 TGAGTAATGAGTATAAATTCGAAACAATTCAAGTACACGGCGGACACACACCGGACGGAGATACACATTCTAGAGCCGTACCTATTTATCAAACGACGTCATACACATTTGATAGCCCGG
Lm04 TAGCTCCATTTTATGCAGATCATGTGGGAAGTATTTTACGCACAAAGGGAATTAAAGACGCACGAGAGAAATTCCAAAGTGGCGAAATAACAGCCTTAGAGTTGCGCAAAATCGAAAATA
Lm05 CTAAGAACCGTCATCTATTTACATCAGAATCGGTTTCTGATGGACATCCAGATAAAATTGCAGATCAAATATCTGATGCAATTTTAGATGCAATTATTTCAAAAGATCCCGACGCGCGTG
Lm06 GATTAGTTCAAACTTGGGGTATCCGAGACTTGGGGAGAAACGTGAATGGAAACGTGCGTTAGAAAAATTCTGGAATGGTGCGATTTCGGAAGAGGAATTGTTGGCTGAAACGAAGGCTCT
Lm07 AAACGTTGTAAAAGAATACACGTCCAGAAACAACAAAGTTCTCGCAGTCGATCATGTCGATTTAGAAATTGAACAAGGCGAGATTTTCGGAGTTGTAGGTTATTCCGGAGCTGGTAAAAG
Li01 TTAGTAGCGGTTATCTCGGTTTTTGCCTTGGTGTTAACGGCTTGCGGAGGCTCTGGCGCTAGTTCAGACAAAGCAAACGGTTCAGGCAAAGCGAAAGACGGCGGCTCTCTAATTATCGGT
Li02 GAGGAAAAAAAGATGAGAAAATTAACAAAAGGGTTAGGAATTTTACTTGCATCAAGCCTTATTCTAGGGTTAGCAGCATGTGGAGGCGGAAGTGACGATAAAGCCTTAAGCACAAAAGAA
Li03 TGAGTAATGAGTATAAATTCGAAACAATTCAAGTACACGGCGGACATACACCGGACGGAGATACGCATTCTAGAGCCGTACCAATTTATCAAACAACATCGTATACATTTGATAGCCCAG
Li04 TGGCACCATTTTATGCAGATCATGTTGGAAGTATTTTACGGACAAAGGCAATTAAAGAGGCACGCGAGAAATTCCAAAGTGGCGAAATTACAACTCAAGAATTACGTGAAATTGAAAATG
Li05 CTAAAAACCGTCATCTATTTACATCGGAATCGGTTTCTGATGGACATCCAGATAAAATTGCAGATCAAATATCTGATGCAATTTTAGATGCAATTATTTCAAAAGATCCGGACGCACGTG
Li06 GATTAGTTCAAACTTGGGGTATCCGAGACTTGGGGAGAAACGTGAATGGAAACGTGCGCTAGAAAAGTTTTGGAATGGTGCGATTTCAGAAGAGGAATTATTGGCGGAAACAAAAGCTCT
Li07 AACGTCGTAAAAGAATATACGTCCAGAAATAACAAAGTTCTCGCAGTCGACCATGTCGATTTAGAAATTGAACAAGGTGAGATTTTCGGAGTAGTTGGTTATTCAGGGGCTGGTAAAAGT
Sa01 TAAATCTAGGGAAATTTATTACAGAATCTGGGGAAGTCATAGATAACTTGCGTTTGAGATATGAGCATGTTGGTTATCATGGACAACCATTAGTTGTAGTTTGTCATGCATTAACTGGCA
Sa02 AGAAGTTGTTAAAGAATATCGGACTAAAAATAAAGAAGTCCTTGCTGTAGATCACGTTAATTTATCGATTCGAGCAGGATCGATTTATGGCGTCATTGGTTTTTCTGGAGCAGGAAAAAG
Sa03 GCAAACTATGTTAAATAACAAACGATTATTTACTTCAGAGTCTGTTACAGAAGGACACCCAGATAAAATCGCTGACCAAGTGTCAGATGCAATATTAGATGCTATTTTAAAAGACGACCC
Sa04 ATGCTTGGGCATTATTCCCCTTGTTATTATTTGTGGCGTTGTTTTTAGGCGTAGGTATTATCACAGGTGATTTTACTTCAATGCCATTAAATGTTGCAATTACGATAACGGTAATTGTGG
Sc01 AGTGCGGCCACAGGGTTCCGCTCGGACCGGTCTTCGCCTGCGAAGAGTGTTTCGGCCCCCTCGAGATCGCCTACGACTTCTCGGACTACGACGCCGAAGAGCTGCGCAAGCGGATCGAAG

Cons .....

Ct01 GCCGGGCAGGAGCCTGATCCGGTGACCGGATCGCGCGCCGTGCCCATTTACCAGACCACCTCCTACGTGTTCGAGAACGCCGAGCACGGCGCTGACCTGTTCGCGCTTCGCAAGGCGGGC

Tt01 AGTCAGTCACTGAAGGGCATCCTGACAAGATCTGTGACCAGATTTCAGATGCCATTTTGGATGAAATTTTAAAAAAAGACCCTTACGCCCGCGTGGCATGTGAGACAGCTGTAACTACCG

Tt02 GTGTAATAAACTTAAAGAAAAGAAATTTGTAATAACTGTGGAAATTTCTCCCCCCAAAGGGATAGATGTAACTAAAACTATCGAGGAAGCTCGAAAACTTAAAGGTGTGGCAGATGCTCT

Tt03 ACTGTTGGGACAGGAGTATTTAAAATAGTTAATTCTAGAGGGAGATATATCAAGGAGAGTACGGGATTTTATCCGGAGATAAAGAAAGTGCTTGTGAAGGATTTGCACAAAAAGAGAAAA

Fn01 GTTTACATACTTTACATCAGAATTTGTTTCACCAGGACATCCAGATAAAATTTCAGATCAAATATCAGATGCAATTTTAGATGCTTGTTTAAAAGATGACCCTAATTCAAGAGTTGCCTG

Fn02 CACTTGAAAATGTAAATAAAATTTATTCCAATAACTTGCATGCTGTAAAAGATGTTAATTTAAAAGTTAATGAAGGAGATATCTTTGGAATTATAGGTTTAAGTGGTGCTGGAAAATCTT

Dr01 ACCGTCCTCCCCCCCAGCCTTGCACTTCGAAGGCGTCAGCAAAACCTACCCCGGCCAGCCGGCGCCGGCGCTGAGCGATTTGACCCTCACCGTTGCGCGCGGCAGCCGCACCGGCATCAT

Dr02 CAGCGCATCCTGATTCTCGACGGCGCCTGGGGTACGCAGCTTCAGCGAGCCAACCTCACCGAAGCGGACTTCCGCTGGGACGAAGCCGACCCCACGCGGATGTACCGGGGCAACTTCGAC

Xa01 CCAACGATTTCGTTGACACCCCCGCCAGCAGCGACGACGGCATCACTGCCGTGCGCGGCGAACTTGTCATCGCCCTGCCGATGCGCCATGCCGGCATGCGCGAGCTGCGGCTGCGCTATG

Xc01 CCACCGCTGACACCTACACGCCCGCCGCTGATAGCGACGCCCCGCCTGCCGTGCGCGGCGAGCTCGTCATCAATCTACCGATGCGCCACGCCGGCCAACGCGAGCTGCGCCTGCGCTACG

Se01 CATTAGAACTAGGTGAGTTTAAAACTGAATCTGGTGAAACGATTGATCATTTACGTCTACGTTATGAACATGTAGGACTTCCTGGTCAACCCCTTGTCGTTGTTTGCCATGCACTTACTG

Se02 ----------

Gs01 CATCGTCGAAGAACAATCCGTCACCTTCGAAACGGATCTCAGGCTGGAAAGCGGCCGGATACTGGGGCCCATCACCCTGGCCTACGAGACCTACGGCCGGCTGAACGCCGACCGGTCCAA

Gs02 GGTCTCGACTGGGATACCCGCACCGGGGCGGTGACGGTACCCATCTACCAGACGGCAACCTTCCGGCATCCGGGATTGGGCCAGAGCACGGGCTACGATTATTCCCGCTCCGGCAACCCC

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Ba02 AAACAAAGTAAATTCATGTGTTTAGGGGGTTATGGAAGTGTATGTAATTAAAAAATTATCGGTTATGGTGTTCACACTATGGGTTATTACGACAGTGACATTTCTAATTATGCATATTAT

Ba03 GAAAATCAAATGAAAAAGAAGTTTGTACCCGGTATTGCATCAGTTGTAGGAGTAAGTATTTTATTAACTGGTTGCGGTAGTTATAAAAACGAAGCAAGCGGAGCAAATGCAAAAGACGAG

Ba04 GGGGAAAAATGATTTCTTTTAATAATGTAAGTAAAGTATATGAATCAGGTGGGCAATCTGTTCATGCGGTGGAGGATGTAACGTTATCAGTTGAGAAAGGCGAAATTTTTGGCATTATCG

Ba05 GACCTATCACAAACATTCGAAAATAATATGTCTCAATTTCCTGGAACACCAAAAATCAATTTAGAAGCCATTACAAGCGTTGAAGAAACAGGTTATCAAGTTACAGATTTCCATTCTGTC

Ba06 TTTGAGGAAGTGTCTGAGAGAATTCAAGCGATGCTTGCTGATATGAAATATGGTTCAATTACAATTGTTGTACAAGATGGAAAAGTCATTCAACTAGAGAAAAGTGAAAAAGTACGTTTA

Ba07 AAAGAAACGAGAGGAAATGGTTTGGCTTTATTACCACTTGGGATATTTTTGGCGCTATTTATAGGTTCTGGAATTATTACAGGTGATTTCTATAAATTGCCGATACTTGTAGCAATTTCA

Ba08 AATATAGAGTAATAAAAGTTGACTATTAAGAGAGGGGAATTATAATGAACAGATTATCAACAAAATTAGTAGTAGCAATCGGAATTGGATCAGCATTATACGGGATATTAGGACTTTGGG

Ba09 CGTCACAAAGAAAAACAATTGAAGAGAGTATCGAAAGAAATAAGGAAAAGTACATAGAAACAAGTCATGATATTCATGCGAATCCGGAGATTGGTAATCAAGAATTTTACGCATCTAGAA

Ba10 GGGGTTGCGAAGTACTGTGACACTCGAAAAATACGTAAAACTGCGTAGTACAGTTTATGAATATATGATAGAGCAAGATAAGCCAATATCATTGTTAGATATTCAAGAACATATCGTTTC

Ba11 GGATATTATTCATTAACAGAAGTAACCGCTGTACAATATGCGAAAGAACATGGTTATTTTGAAAAGAAAGCAAATGTAGTTTGTCATGAAATTGGAGATGGAAATTTAAATTATGTGTTC

Ba12 ATTTAATCCATGATGATTCACATAACTTAGAAAAAAAAGCTGAGCAAATTGCACTCGGTTTAACAATTGGCTCTTGGACTCATTTGCCACACTTATTGCAAGAACAGTTAAAGCAGCATA

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Ba14 TCAAAAGGAATTGTAATAGGTGATGGTGCGGTTGGAACATTATTACATTCACACGGTTTGCAAAGTAGTTTTGAAGAATTGAATATATCTGATCCAGATTTAATTATATCGATTCATAAG
Ba15 AATTAAGGATGAGTTCCGTACAATATATACAATTACTGTAGGGAGGTTTACCACATGACAAAAAAACGTCATCTGTTCACATCTGAGTCTGTAACTGAAGGACATCCAGATAAAATTTGT
Ba16 ACGGTGGGCTACCGTATCAAAAATAAAAAATTGCGGAGTCAATCAAAAATCTAGCTCCAGCGGCTAGAACAGTCGGTCGTTTCATCCCTTCCTATGAGGCAAAAAGCGCCTCTAAGTCTG
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Bc01 GGGAAAAAATGATTTCTTTTAACAATGTAAGTAAAGTATATGAAACAGGTGGGCAATCTGTTCATGCGGTGGAGGATGTAACATTATCAGTTGAGAAAGGCGAAATTTTTGGCATTATCG
Bc02 TGGTTGCCGATTTTTGGGGGATGGCTTCGGAATGTAAATGATGAATCTATGCCGCCTACGTTTGAGTATGCAAAACAAACGGCGCAAGCGGCAGAACAATTAGGTTTTTCAACAACACTT
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Bc07 TAGAAAGTTTTCCGCAATTATTTAAGTATGTATACATAACTTTAGGAATTACTGTAGTTTCAATGATTATTTCTTTTGTTATAGGGATAGGTTTGGCGATCATAACGAAAAACAAAACGA
Bc08 GGTTGCGCATTACTGTGACACTCGAAAAATACGTCAAACTGCGTAGTACAGTTTATGAATATATGATAGAGCAAGATAAGCCAATATCATTGTTAGATATTCAAGAACATATCGTTTCGC
Bc09 ATTTAATCCATGATGATTCACATAACTTAGAAAAAAAAGCTGAGCAAATTGCACTCGGTTTAACAATTGGCTCTTGGACTCATTTGCCACATTTATTGCAAGAACAATTAAAGCAGCATA
Bc10 TCAAAAGGAATTGTAATAGGTGATGGTGCGGTTGGGACGTTATTACATTCACATGGTTTACAAAGTAGTTTTGAAGAATTGAATATATCTGATCCAGATTTAATTATATCGATTCATAAG
Bc11 ACATGTCAACTATCGAAACAAAATTAGCGCAAATCGGAAACCGGAGTGAAACTACAACAGGAACTGTTAATCCACCTGTTTATTTTTCAACTGCTTATCGTCACGAAGGAATTGGTAAAT
Bc12 GGGATATTATGCATTAACTGAAACAACAGCTATACAATATGCGAAAGAACACGGTTATTTTGAAAAGAAAGCAAATGTATTTTGTCATGAAATTGGAGATGGAAATTTAAATTACGTGTT
Bc13 AATTAAGGATGAGTTCCGTACAATATATACAATTACTGTAGGGAGGTTTACCACATGACAAAAAAACGTCATCTGTTCACATCTGAGTCTGTAACTGAAGGACATCCAGATAAAATTTGT
Bc14 ACGGTGGACTACACGCATTAAACATAAAAAATTGCGGAGTCGATCCAAACAAAAAAGGGGTGATACACCATGATTCTATTAGAGAATGTAAAGAAAATATATAAAGCAAAAAGCGGTGAT
Bc15 GGAAAGGAACAATTTGCGTGCAAGGTGGCTATACGCCAAAGAATGGTGAACCGCGTGTTTTACCGCTTTATCAAAGTACAACGTATAAATACGATACTTCGGATGATTTAGCAGCCTTAT
Bc16 GAAAATCAAATGAAAAAAAAAGTTTGTACCCGGTATTGCATCAGTTGTAGGAGTAAGTATTTTATTAACTGGTTGCGGTAGTTATAAAAACGAAGCAAGCGGAGCAAATGCAAAAGACGAG
Bc17 TATTAAGCATTGTAAGTGGGGCTGTATTATTATTAAGCGCATGTAGCGGGAGTTCAGATAAAGAAGTAAAAGCGTTAGATGAGAAAAAGATTACTGTCGGTGTAACAGGAGGGCCTCATG
Bc18 AAACTAAGTAAATATATGTGTTTAGGGGGTTATTGGAGTGTATGTAATTAAAAAATTATCAGTTATGGTGTTCACGCTATGGGTTATTACGACGGTGACATTTCTAATTATGCATATTAT

B. Cobalamin Riboswitch Alignment.

ID		Start	End	Accession	Organism
Atu01	+	70441	70625	NC_003304.1	Agrobacterium tumefaciens
Atu02	-	441331	441136	NC_003305.1	Agrobacterium tumefaciens
Atu03	+	877645	877833	NC_003304.1	Agrobacterium tumefaciens
Atu04	+	921717	921886	NC_003305.1	Agrobacterium tumefaciens
Atu05	-	1640563	1640420	NC_003304.1	Agrobacterium tumefaciens
Atu06	-	2810076	2809899	NC_003304.1	Agrobacterium tumefaciens
Bha01	-	466904	466746	NC_002570.1	Bacillus halodurans
Bha02	+	528894	529051	NC_002570.1	Bacillus halodurans
Bha03	+	870599	870748	NC_002570.1	Bacillus halodurans
Bha04	+	1661078	1661219	NC_002570.1	Bacillus halodurans
Bsu01	-	3403719	3403620	NC_000964.1	Bacillus subtilis
Bja01	+	2232813	2232975	NC_004463.1	Bradyrhizobium japonicum
Bja02	+	3617311	3617490	NC_004463.1	Bradyrhizobium japonicum
Bja03	+	3630677	3630857	NC_004463.1	Bradyrhizobium japonicum
Bja04	+	3634122	3634284	NC_004463.1	Bradyrhizobium japonicum
Bja05	-	5279669	5279495	NC_004463.1	Bradyrhizobium japonicum
Bme01	+	679030	679218	NC_003317.1	Brucella melitensis chromosome I
Bme02	+	717388	717585	NC_003317.1	Brucella melitensis chromosome I

Bme03 + 559758 559950 NC_003318.1 Brucella melitensis chromosome II

Bme04 - 973106 972933 NC_003318.1 Brucella melitensis chromosome II

Ccr01 + 502968 503156 NC_002696.2 Caulobacter crescentus

Ccr02 + 1925017 1925166 NC_002696.2 Caulobacter crescentus

Cte01 - 409802 409630 NC_002932.3 Chlorobium tepidum

Cte02 + 422045 422244 NC_002932.3 Chlorobium tepidum

Cte03 + 443769 443951 NC_002932.3 Chlorobium tepidum

Cte04 + 584183 584411 NC_002932.3 Chlorobium tepidum

Cte05 + 882576 882770 NC_002932.3 Chlorobium tepidum

Cac01 + 1509969 1510116 NC_003030.1 Clostridium acetobutylicum

Cac02 + 2557903 2558041 NC_003030.1 Clostridium acetobutylicum

Cpe01 + 248269 248429 NC_003366.1 Clostridium perfringens

Cpe02 + 1241749 1241887 NC_003366.1 Clostridium perfringens

Cpe03 - 1431291 1431152 NC_003366.1 Clostridium perfringens

Cpe04 - 1549481 1549348 NC_003366.1 Clostridium perfringens

Eco01 + 4160983 4161133 NC_000913.1 Escherichia coli

Fnu01 + 934517 934658 NC_003454.1 Fusobacterium nucleatum

Lig01 + 1347854 1347994 NC_004342.1 Leptospira interrogans chromosome I

Lmo01 + 1179829 1179979 NC_003210.1 Listeria monocytogenes

Mlo01 - 1101076 1100918 NC_002678.1 Mesorhizobium loti

Mlo02	+	1149143	1149308	NC_002678.1	Mesorhizobium loti
Mlo03	-	4044577	4044416	NC_002678.1	Mesorhizobium loti
Mlo04	-	4957334	4957164	NC_002678.1	Mesorhizobium loti
Mlo05	-	6170855	6170715	NC_002678.1	Mesorhizobium loti
Mlo06	+	6749148	6749315	NC_002678.1	Mesorhizobium loti
Mle01	-	1130394	1130222	NC_002677.1	Mycobacterium leprae
Mtu01	-	309822	309703	NC_000962.1	Mycobacterium tuberculosis
Mtu02	-	1261701	1261497	NC_000962.1	Mycobacterium tuberculosis
Pae01	+	1381520	1381688	NC_002516.1	Pseudomonas aeruginosa
Pae02	-	3261415	3261204	NC_002516.1	Pseudomonas aeruginosa
Pae03	+	3265563	3265728	NC_002516.1	Pseudomonas aeruginosa

ID	Start	End	Accession	Organism
Pae04	-	3305780	3305629	NC_002516.1 Pseudomonas aeruginosa
Ppu01	-	2765203	2765045	NC_002947.3 Pseudomonas putida
Ppu02	-	2768953	2768785	NC_002947.3 Pseudomonas putida
Ppu03	+	3857563	3857746	NC_002947.3 Pseudomonas putida
Ppu04	-	3981958	3981816	NC_002947.3 Pseudomonas putida
Rso01	-	2609233	2609017	NC_003295.1 Ralstonia solanacearum
Sme01	+	954780	954943	NC_003047.1 Sinorhizobium meliloti
Sme02	-	1999747	1999574	NC_003047.1 Sinorhizobium meliloti
Sme03	-	2122891	2122516	NC_003047.1 Sinorhizobium meliloti
Sme04	+	66265	66456	NC_003078.1 Sinorhizobium meliloti plasmid pSymB
Sme05	+	580403	580578	NC_003078.1 Sinorhizobium meliloti plasmid pSymB
Sco01	+	1037869	1038053	NC_003888.1 Streptomyces coelicolor
Sco02	+	1045899	1046106	NC_003888.1 Streptomyces coelicolor
Sco03	+	1051420	1051563	NC_003888.1 Streptomyces coelicolor
Sco04	-	5688395	5688291	NC_003888.1 Streptomyces coelicolor
Sco05	-	6532337	6532191	NC_003888.1 Streptomyces coelicolor
Sfl01	+	4183416	4183566	NC_004337.1 Shigella flexneri (*)
Son01	+	826836	827026	NC_004347.1 Shewanella oneidensis

Son02 + 1071692 1071874 NC_004347.1 Shewanella oneidensis

Sti01 - 2114053 2113918 NC_003197.1 Salmonella typhimurium

Sti02 + 4347871 4348024 NC_003197.1 Salmonella typhimurium

Tma01 - 84288 84144 NC_000853.1 Thermotoga maritima

Tte01 + 395153 395353 NC_003869.1 Thermoanaerobacter tengcongensis

Tte02 + 396075 396275 NC_003869.1 Thermoanaerobacter tengcongensis (*)

Vch01 + 145142 145306 NC_002505.1 Vibrio cholerae chromosome I

Vvu01 + 1165724 1165882 NC_004459.1 Vibrio vulnificus chromosome I

Xac01 - 3631166 3630987 NC_003902.1 Xanthomonas campestris

Xax01 - 3758428 3758245 NC_003919.1 Xanthomonas citri

Ype01 - 4393235 4393008 NC_003143.1 Yersinia pestis

Aca01 - 340 170 M34485.1 Acinetobacter calcoaceticus

Avi01 - 388 214 U45329.1 Agrobacterium vitis

Bfr01 + 580 762 AY043208.1 Bacteroides fragilis

Bmg01 + 1211 1350 AJ000758.1 Bacillus megaterium

Lma01 - 76392 76234 AL499620.1 Leishmania major

Pfr01 - 543 373 AY033236.1 Propionibacterium freudenreichii

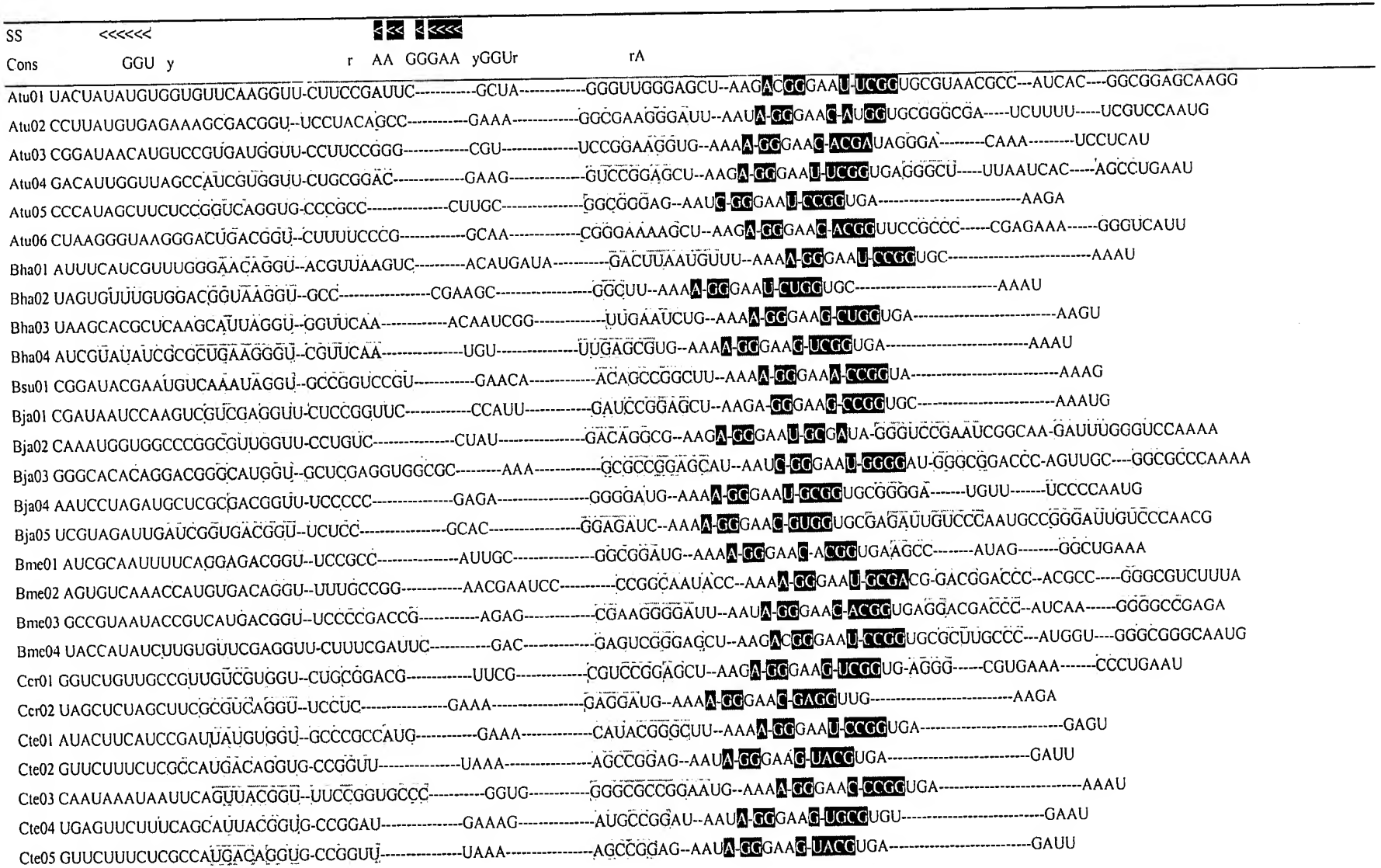
Rca01 + 105327 105521 AF010496.1 Rhodobacter capsulatus

Rca02 + 116991 117174 AF010496.1 Rhodobacter capsulatus

Rca03 - 39849 39672 AF010496.1 Rhodobacter capsulatus

Rsp01	+	201	341	B07728.1	Rhodobacter sphaeroides
Sbi01	-	330	147	BH245584.1	Sorghum bicolor
Sgi01	-	9209	9035	AF263012.1	Streptomyces griseus
Svi01	-	1235	1052	U27616.3	Stealth virus 1
Zmo01	-	24942	24808	AF193754.1	Zymomonas mobilis
Zmo02	-	4323	4162	AF193754.1	Zymomonas mobilis

Accession numbers are for Genbank sequence entries. Start and end positions are the 5' and 3' nucleotides of the first interior UG base pair of stem P1 (orange). Secondary structure (SS) and sequence consensus (Cons) lines are shown above the alignment. In the consensus sequence, uppercase and lowercase letters represent ≥90% and ≥80% conservation at a position, respectively. The degenerate bases R (A,G) and Y (C,U) appear only when a single base is not 80% conserved. Sequences marked with an asterisk (*) were excluded when determining the sequence consensus because they have >90% identity to another sequence in the alignment.


SS <<<<<< <<< <<<<
Cons GGU y r AA GGGAA yGGUr rA
Atu01 UACUAUAUGUGGUGUUCAAGGUU-CUUCCGAUUC----------GCUA----------GGGUUGGGAGCU--AAGACGGGAAU-UCGGUGCGUAACGCC---AUCAC----GGCGGAGCAAGG
Atu02 CCUUAUGUGAGAAAGCGACGGU--UCCUACAGCC----------GAAA----------GGCGAAGGGAUU--AAUA-GGGAAG-AUGGUGCGGGCGA-----UCUUUU-----UCGUCCAAUG
Atu03 CGGAUAACAUGUCCGUGAUGGUU-CCUUCCGGG----------CGU----------UCCGGAAGGUG--AAAA-GGGAAG-ACGAUAGGGA---------CAAA---------UCCUCAU
Atu04 GACAUUGGUUAGCCAUCGUGGUU-CUGCGGAC----------GAAG----------GUCCGGAGCU--AAGA-GGGAAU-UCGGUGAGGGCU-----UUAAUCAC-----AGCCUGAAU
Atu05 CCCAUAGCUUCUCCGGUCAGGUG-CCCGCC----------CUUGC----------GGCGGGAG--AAUG-GGGAAU-CCGGUGA----------AAGA
Atu06 CUAAGGGUAAGGGACUGACGGU--CUUUUCCCG----------GCAA----------CGGGAAAAGCU--AAGA-GGGAAC-ACGGUUCCGCCC------CGAGAAA------GGGUCAUU
Bha01 AUUUCAUCGUUUGGGAACAGGU--ACGUUAAGUC----------ACAUGAUA----------GACUUAAUGUUU--AAAA-GGGAAU-CCGGUGC----------AAAU
Bha02 UAGUGUUUGUGGACGGUAAGGU--GCC----------CGAAGC----------GGCUU--AAAA-GGGAAU-CUGGUGC----------AAAU
Bha03 UAAGCACGCUCAAGCAUUAGGU--GGUUCAA----------ACAAUCGG----------UUGAAUCUG--AAAA-GGGAAG-CUGGUGA----------AAGU
Bha04 AUCGUAUAUCGCGCUGAAGGGU--CGUUCAA----------UGU----------UUGAGCGUG--AAAA-GGGAAG-UCGGUGA----------AAAU
Bsu01 CGGAUACGAAUGUCAAAUAGGU--GCCGGUCCGU----------GAACA----------ACAGCCGGCUU--AAAA-GGGAAA-CCGGUA----------AAAG
Bja01 CGAUAAUCCAAGUCGUCGAGGUU-CUCCGGUUC----------CCAUU----------GAUCCGGAGCU--AAGA-GGGAAG-CCGGUGC----------AAAUG
Bja02 CAAAUGGUGGCCCGGCGUUGGUU-CCUGUC----------CUAU----------GACAGGCG--AAGA-GGGAAU-GCGAUA-GGGUCCGAAUCGGCAA-GAUUUGGGUCCAAAA
Bja03 GGGCACACAGGACGGGCAUGGU--GCUCGAGGUGGCGC---------AAA----------GCGCCGGAGCAU--AAUC-GGGAAU-GGGGAU-GGGCGGACCC-AGUUGC----GGCGCCCAAAA
Bja04 AAUCCUAGAUGCUCGCGACGGUU-UCCCCC----------GAGA----------GGGGAUG--AAAA-GGGAAU-GCGGUGCGGGGA-------UGUU-------UCCCCAAUG
Bja05 UCGUAGAUUGAUCGGUGACGGU--UCUCC----------GCAC----------GGAGAUC--AAAA-GGGAAC-GUGGUGCGAGAUUGUCCCAAUGCCGGGAUUGUCCCAACG
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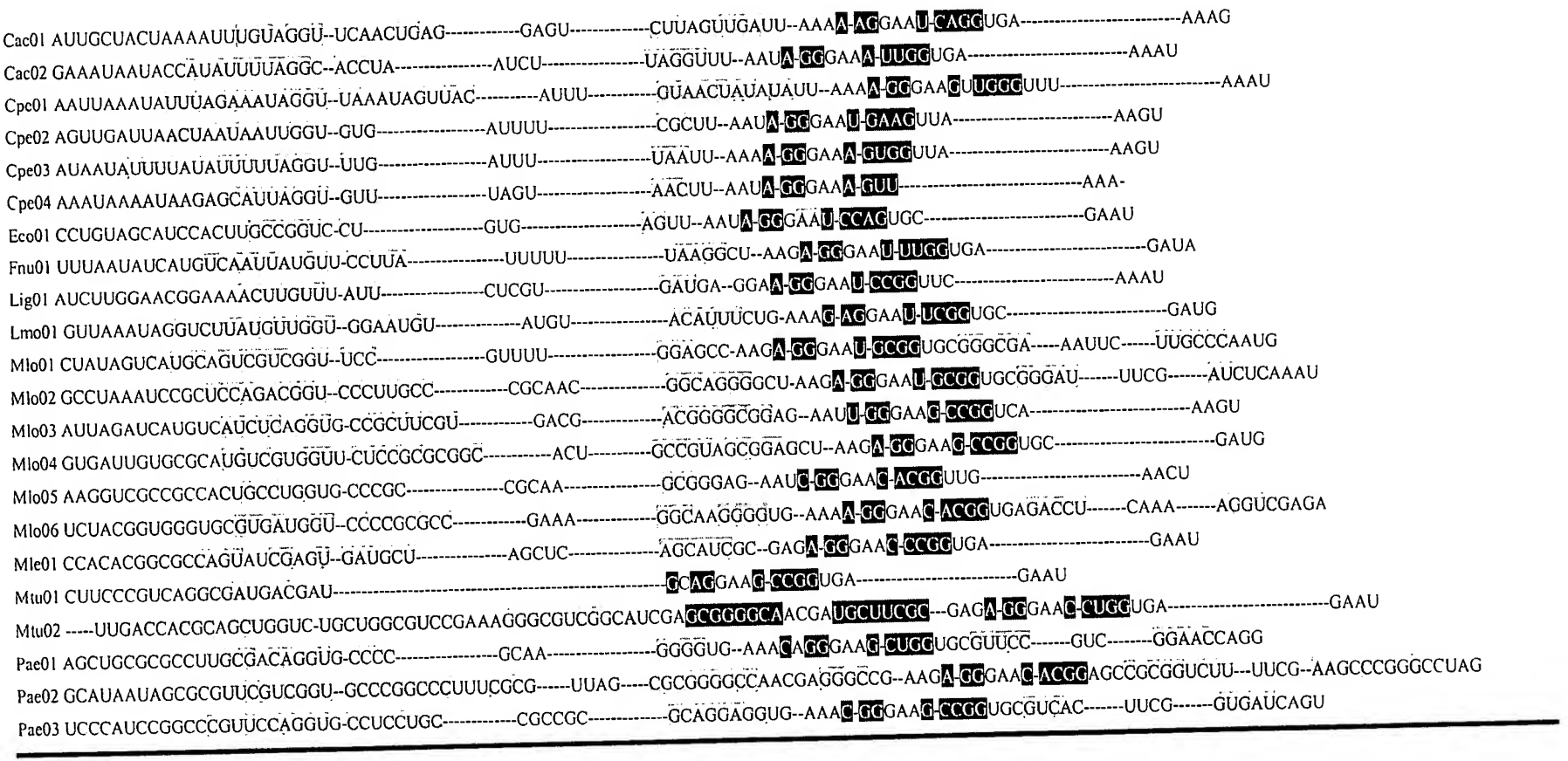
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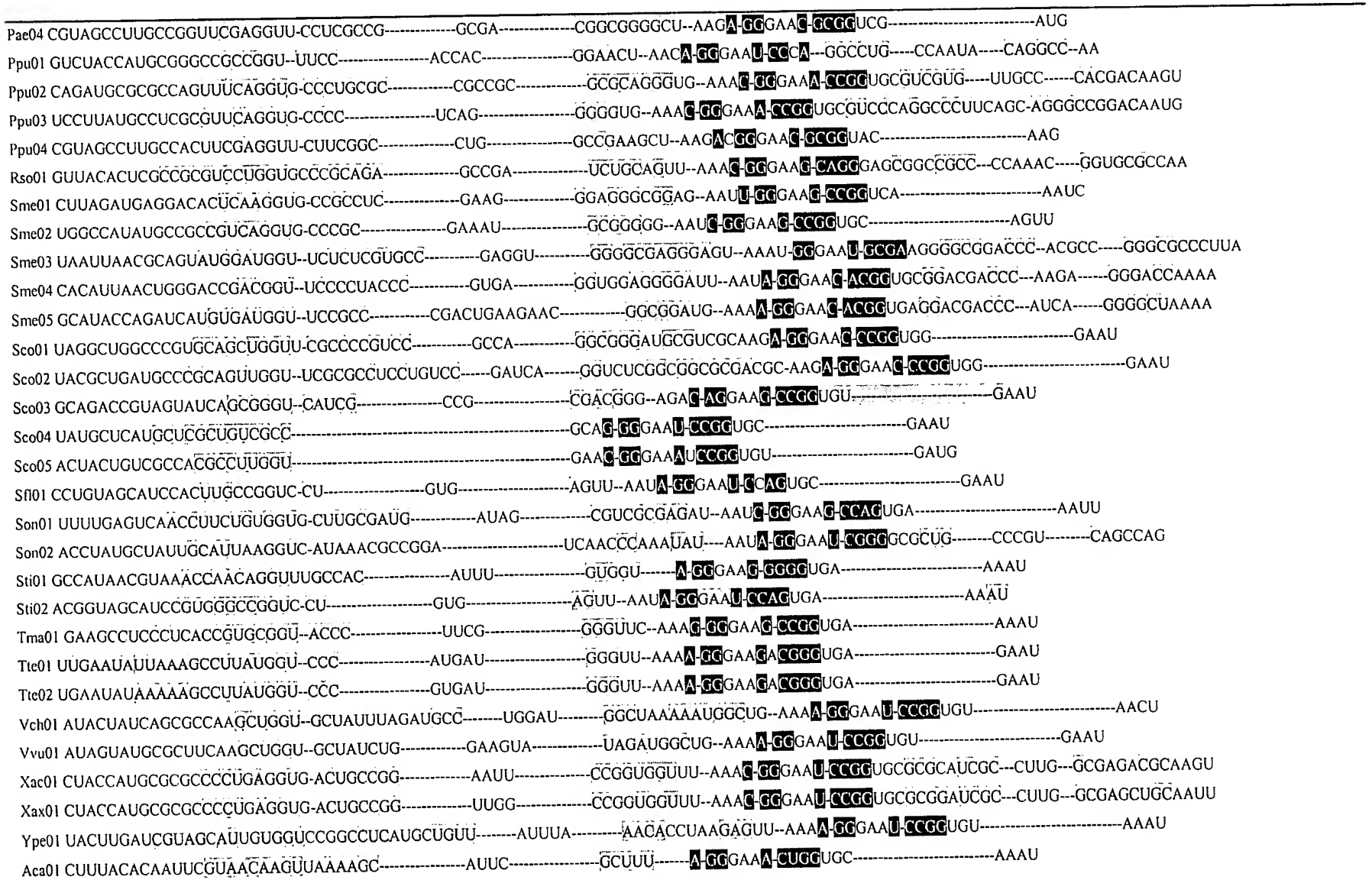
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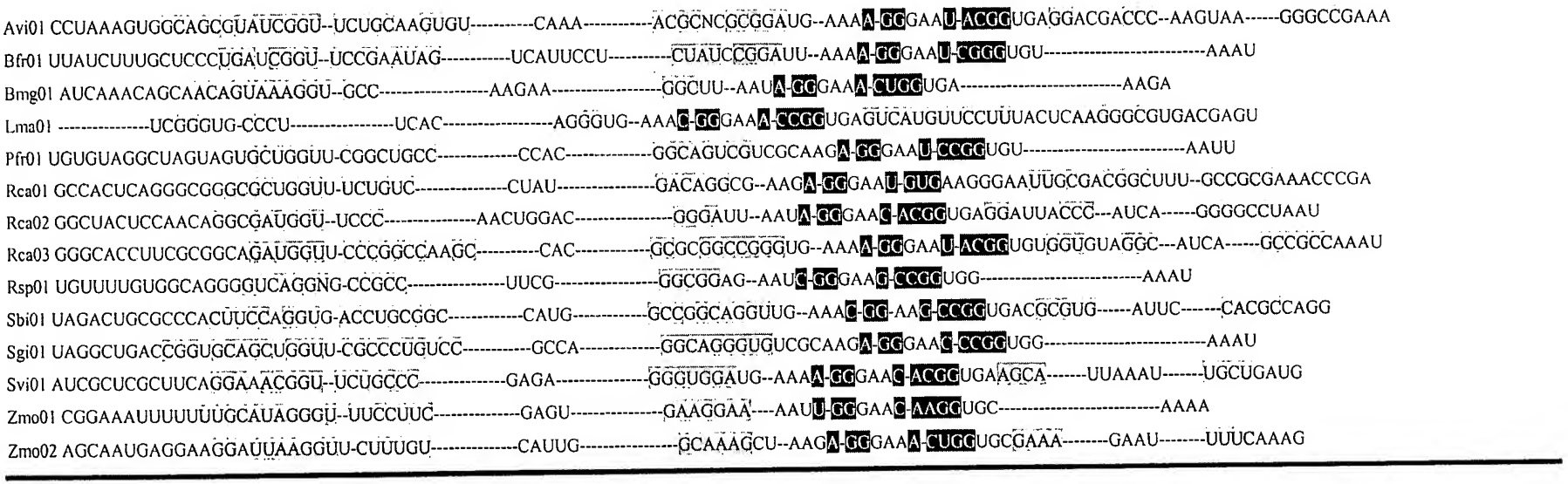
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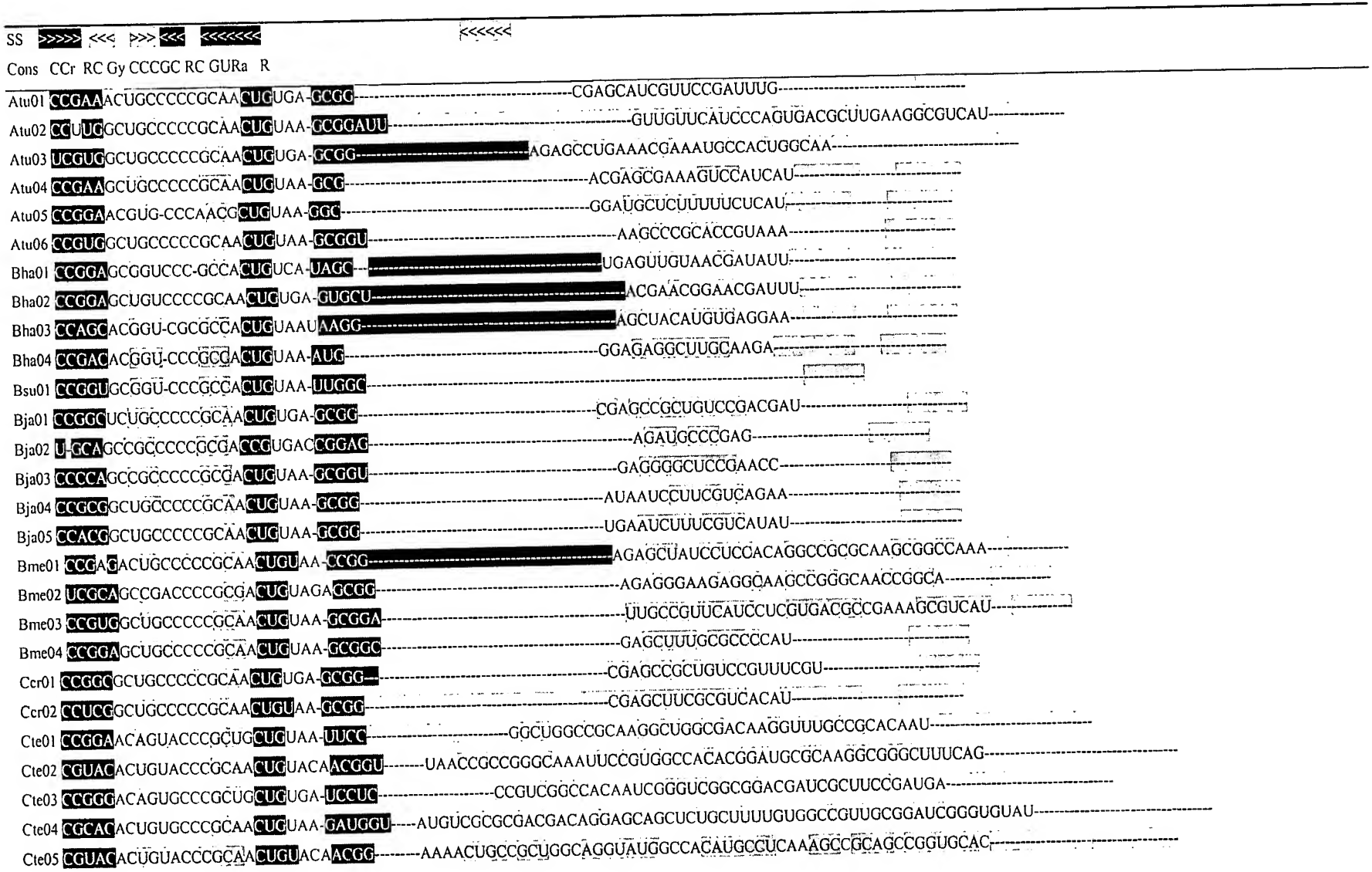
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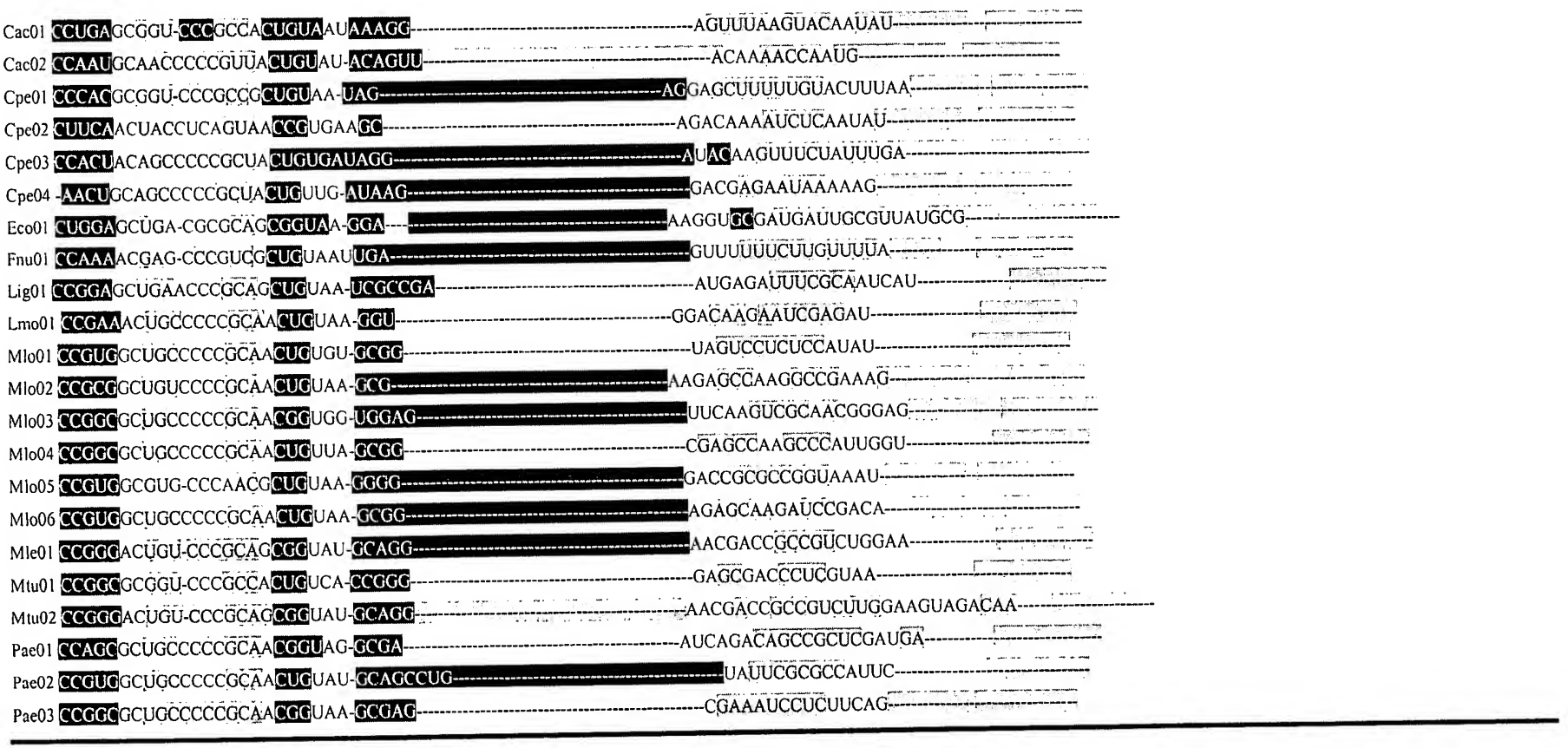
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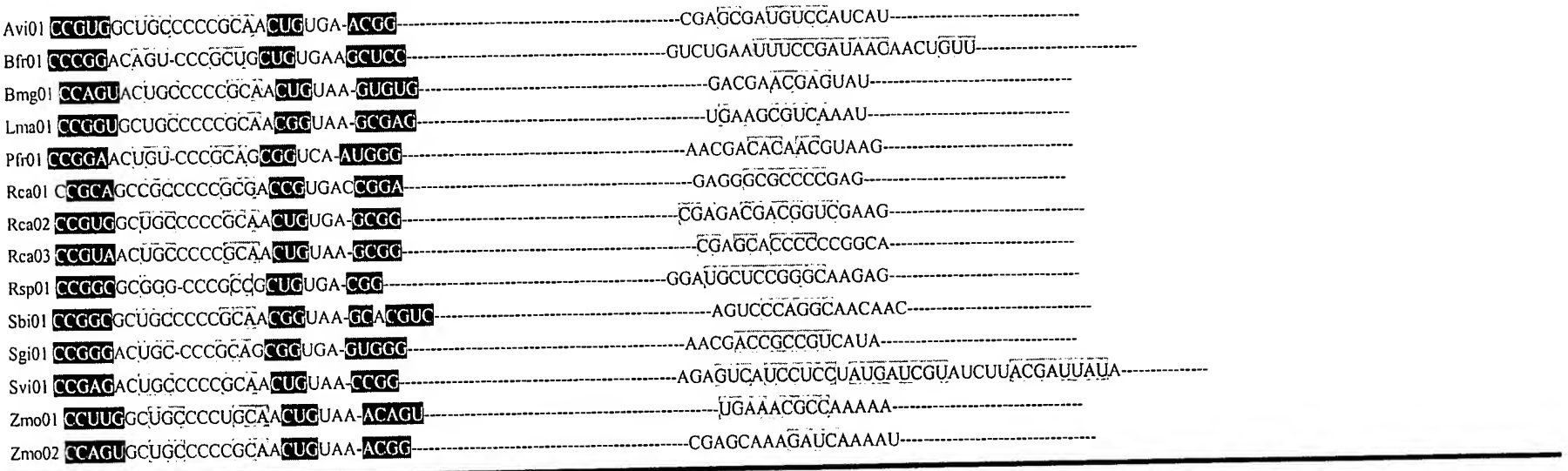
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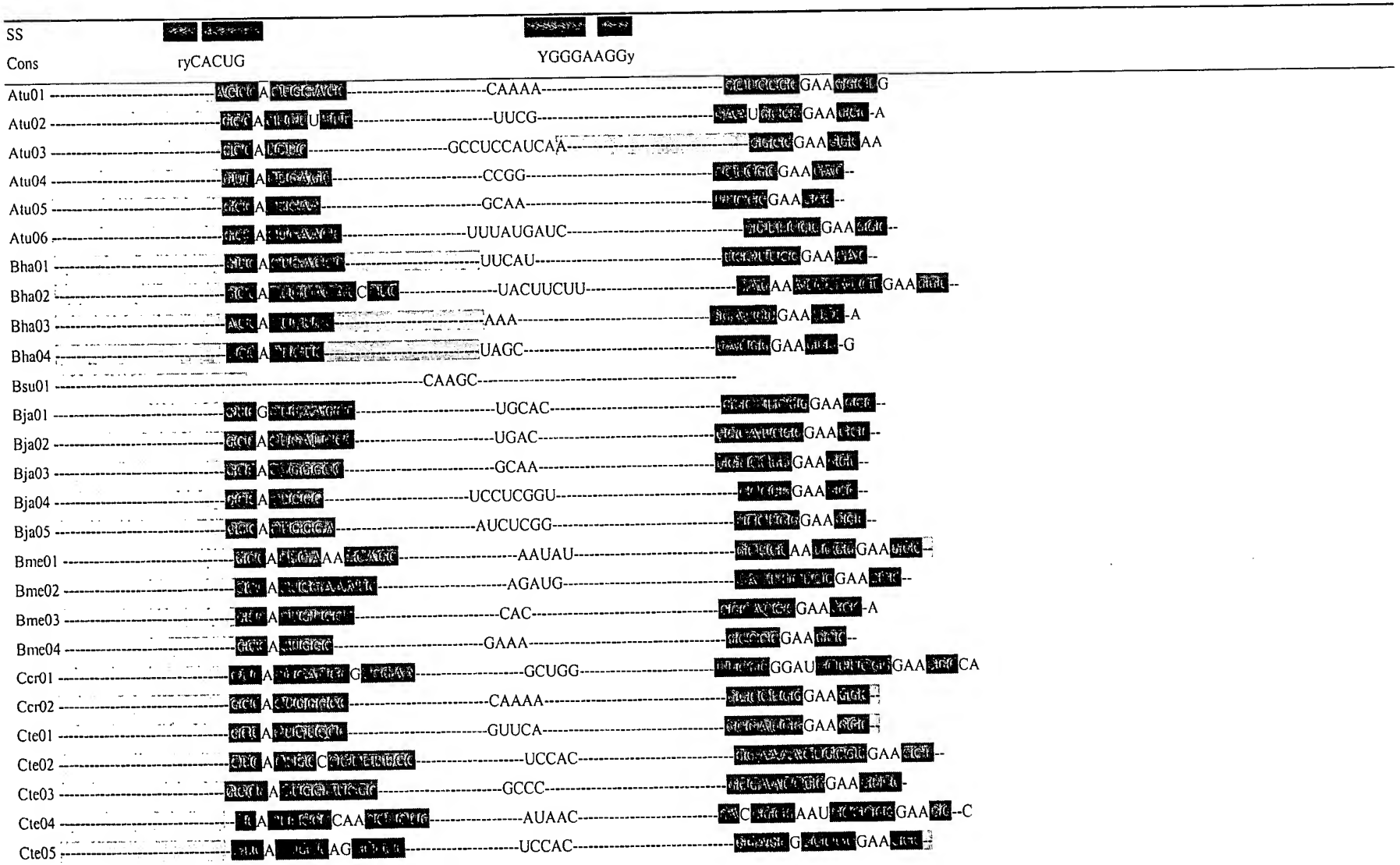
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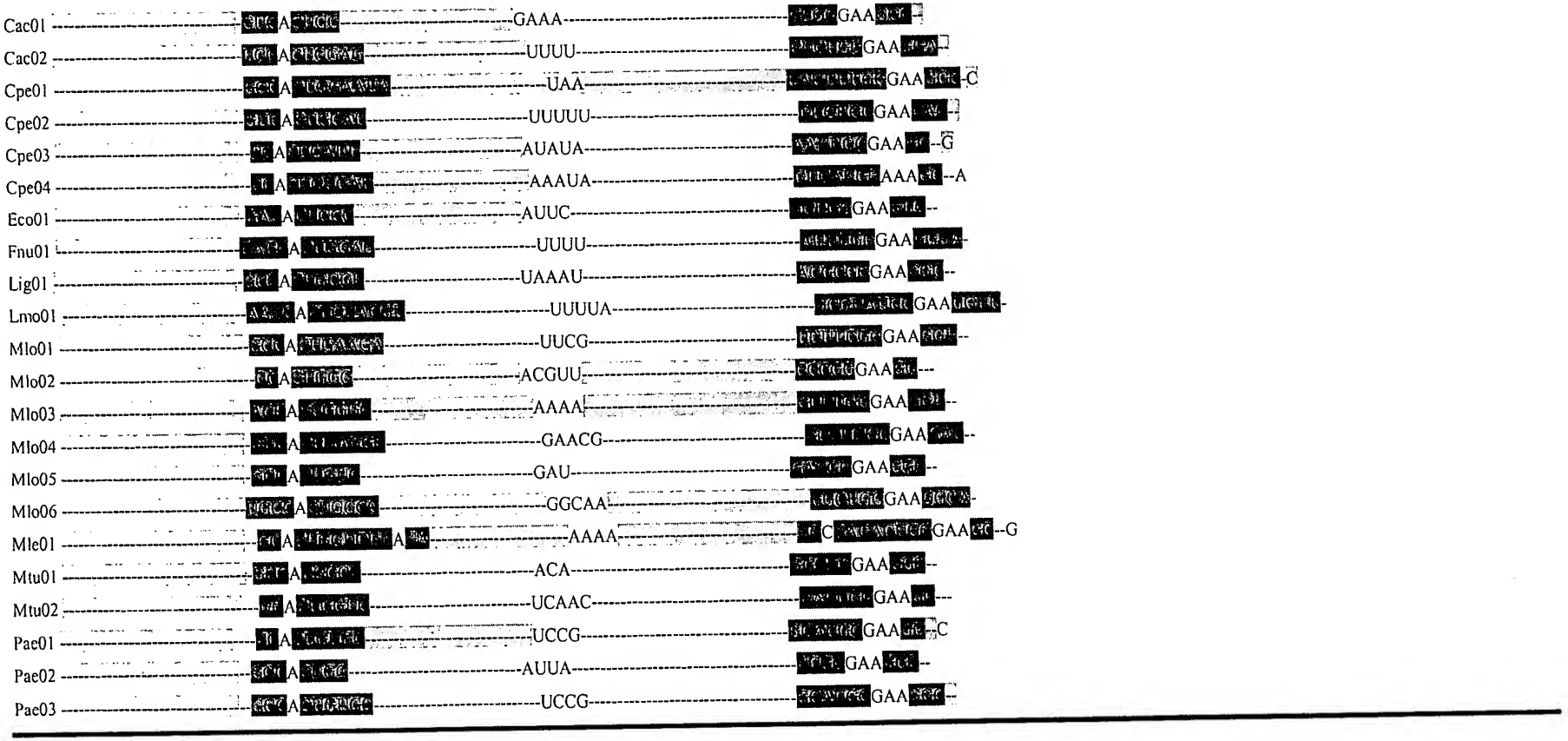
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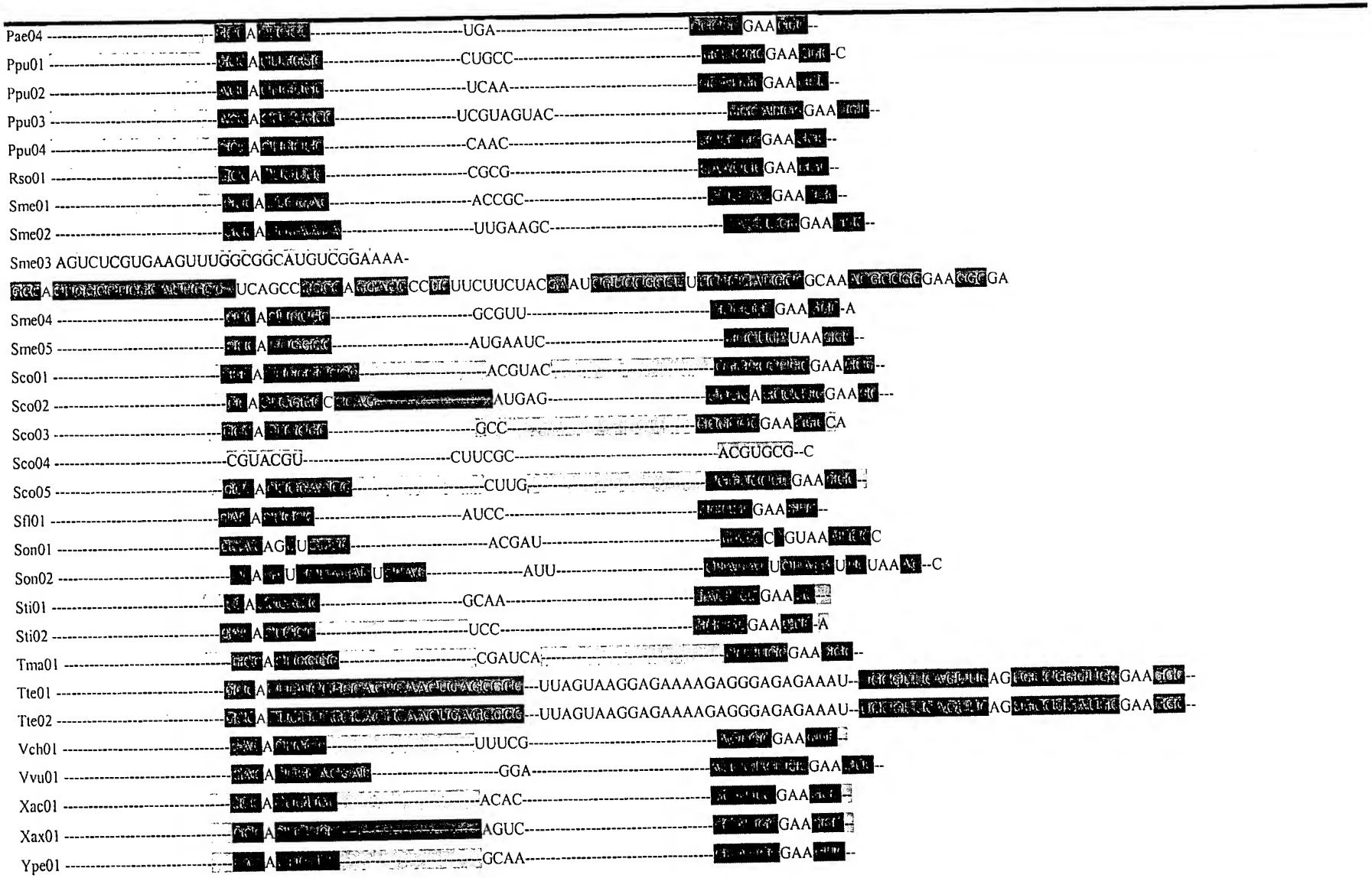
Mtu01
Mtu02
Pae01
Pae02
Pae03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Sco02
Sco03
Sco04
Sco05
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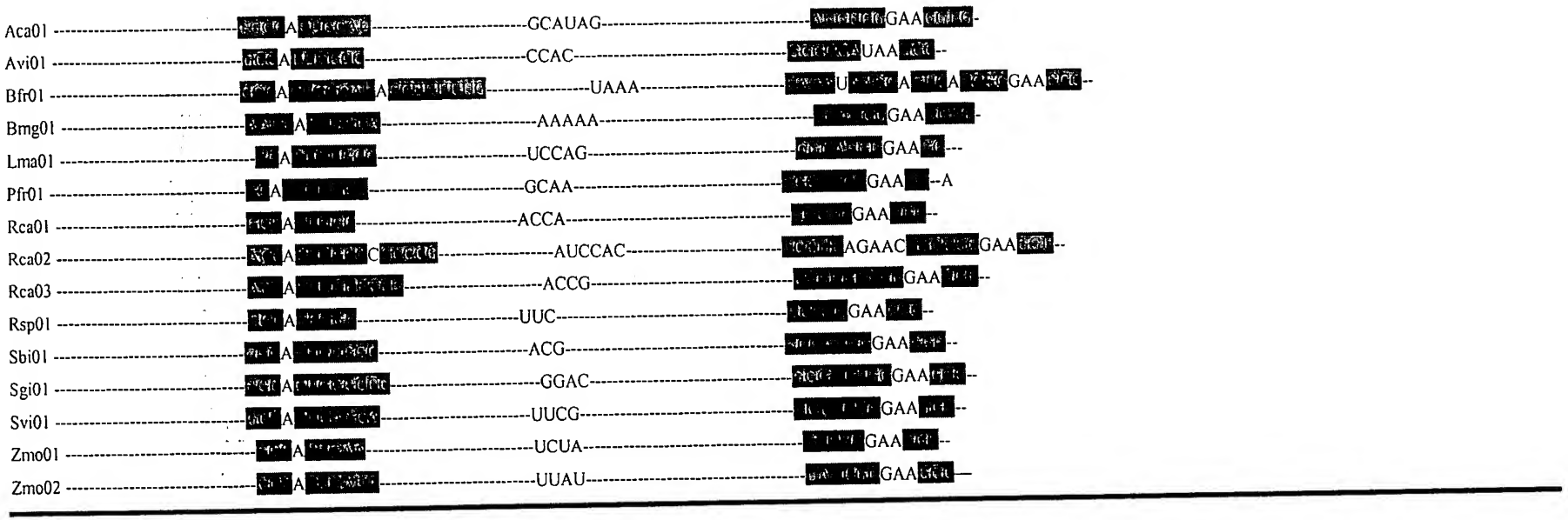
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Lma01
Pfr01
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Rca02
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Zmo01
Zmo02
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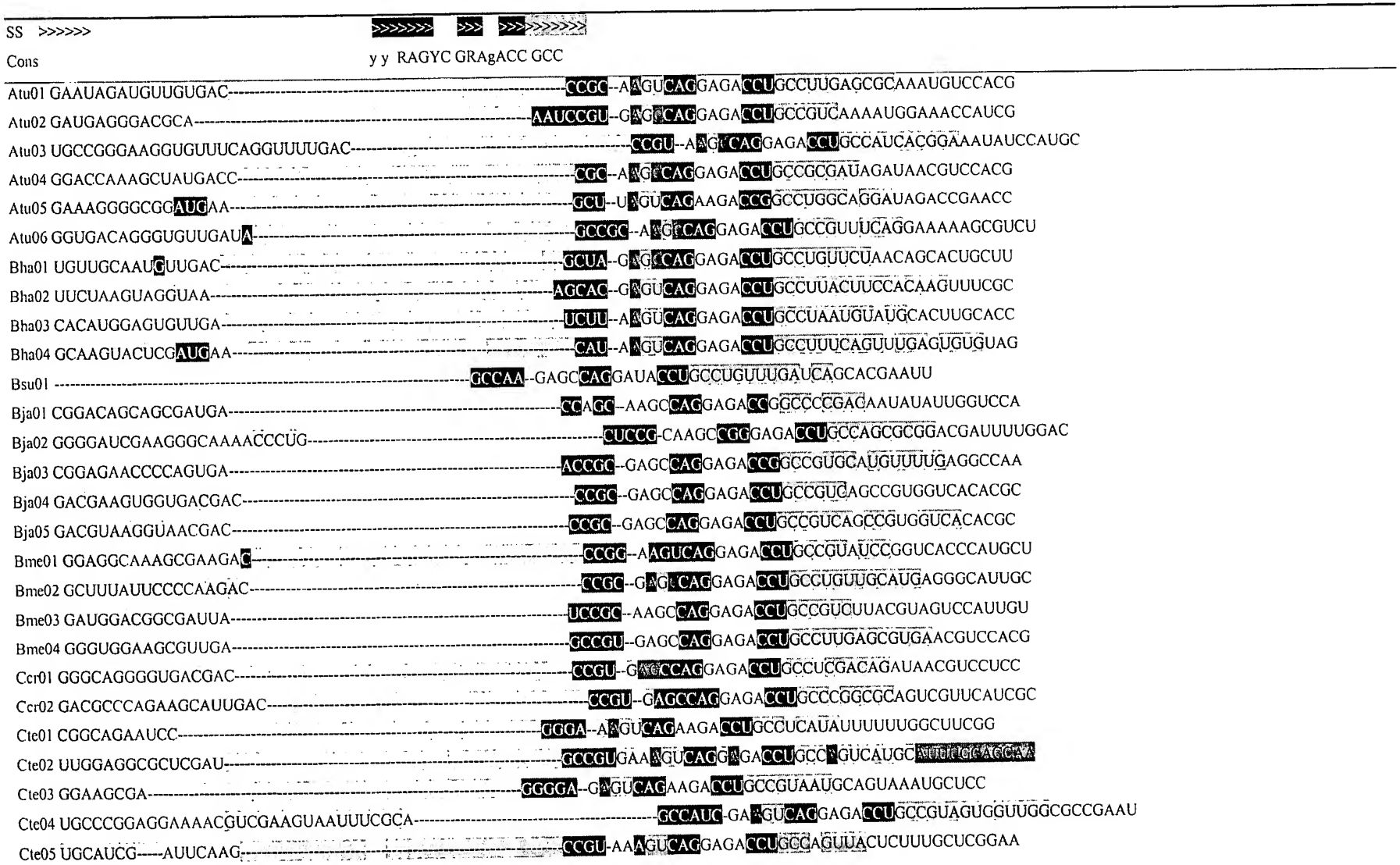
SS >>>>>>
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Bsu01
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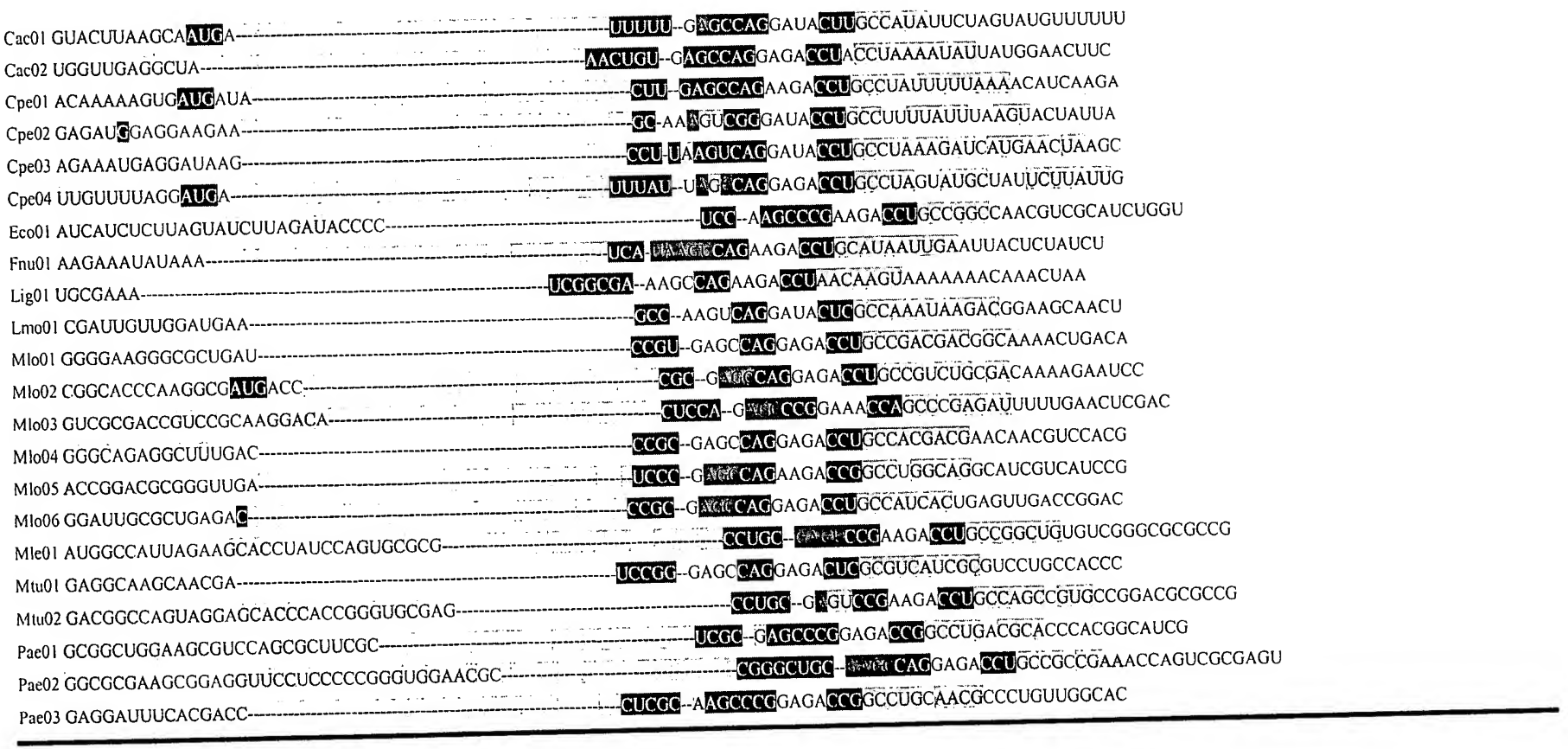
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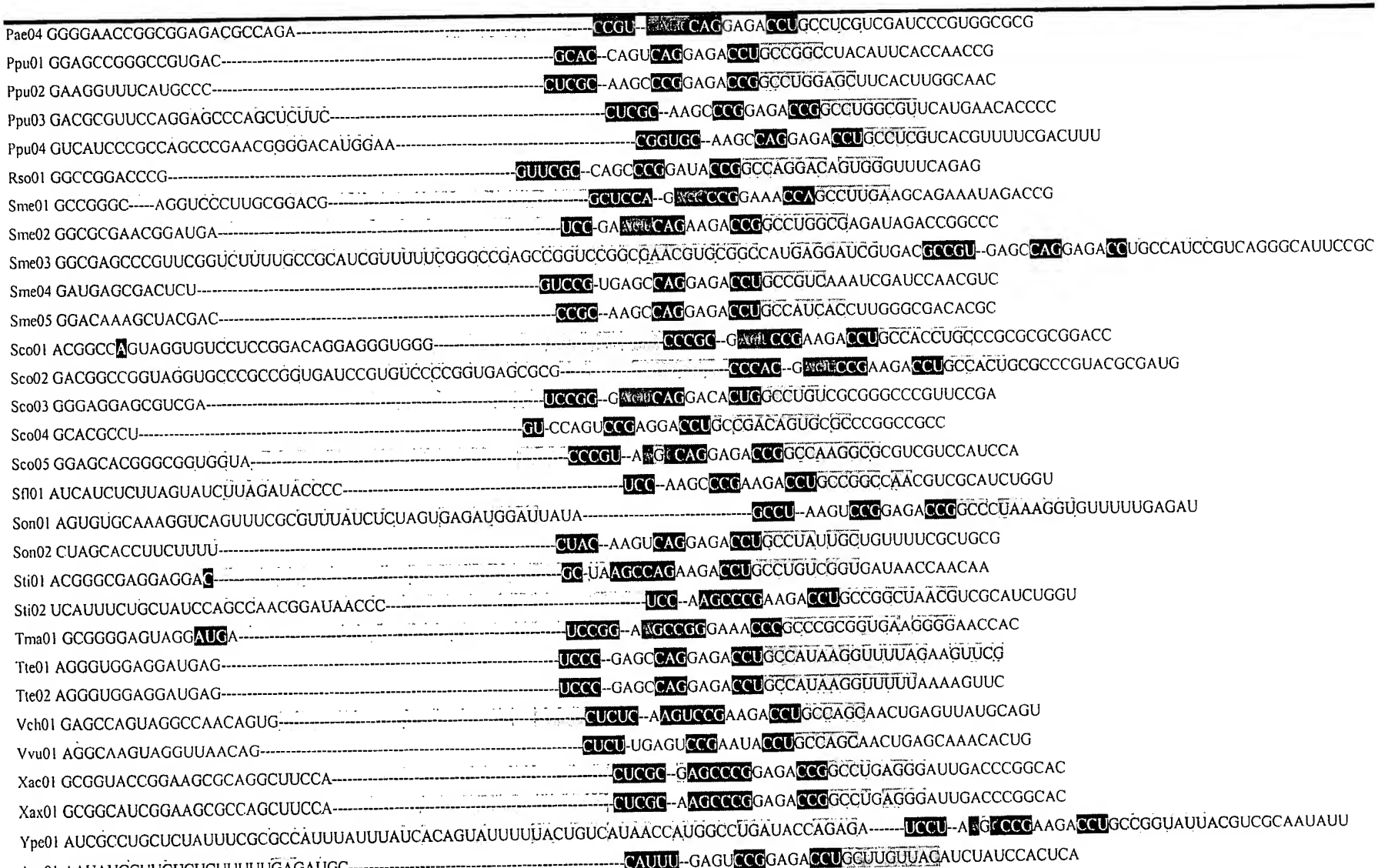
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Sfl01 AUCAUCUCUUAGUAUCUUAGAUACCCC----------UCC--AAGCCCGAAGACCUGCCGGCCAACGUCGCAUCUGGU
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Sti02 UCAUUUCUGCUAUCCAGCCAACGGAUAACCC----------UCC--AAGCCCGAAGACCUGCCGGCUAACGUCGCAUCUGGU
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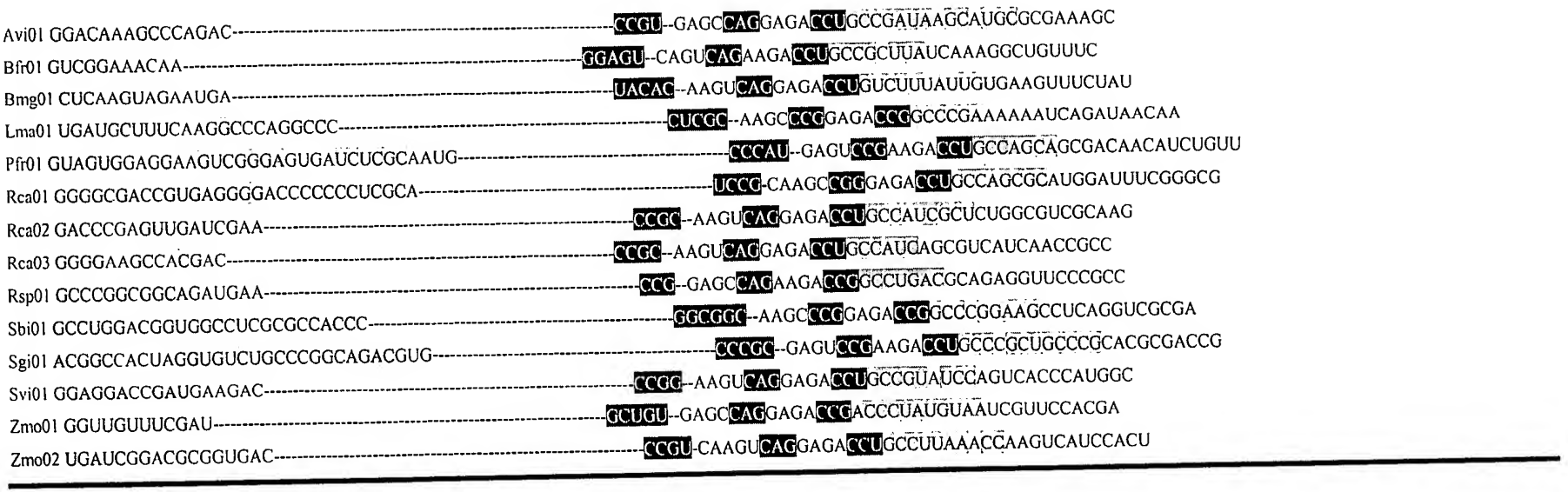
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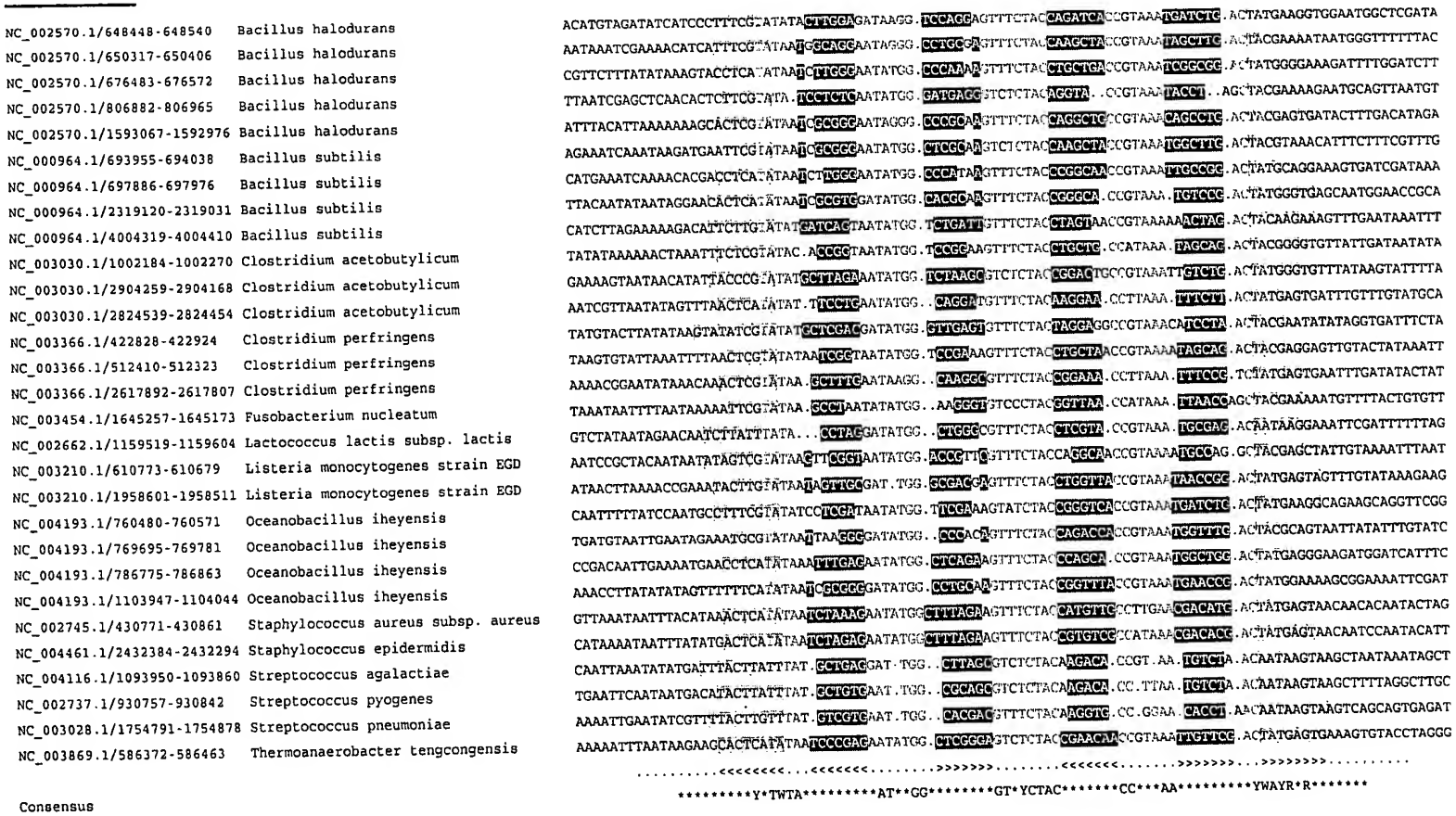
C. G-Box


NC_002570.1/648448-648540 Bacillus halodurans
NC_002570.1/650317-650406 Bacillus halodurans
NC_002570.1/676483-676572 Bacillus halodurans
NC_002570.1/806882-806965 Bacillus halodurans
NC_002570.1/1593067-1592976 Bacillus halodurans
NC_000964.1/693955-694038 Bacillus subtilis
NC_000964.1/697886-697976 Bacillus subtilis
NC_000964.1/2319120-2319031 Bacillus subtilis
NC_000964.1/4004319-4004410 Bacillus subtilis
NC_003030.1/1002184-1002270 Clostridium acetobutylicum
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NC_003366.1/422828-422924 Clostridium perfringens
NC_003366.1/512410-512323 Clostridium perfringens
NC_003366.1/2617892-2617807 Clostridium perfringens
NC_003454.1/1645257-1645173 Fusobacterium nucleatum
NC_002662.1/1159519-1159604 Lactococcus lactis subsp. lactis
NC_003210.1/610773-610679 Listeria monocytogenes strain EGD
NC_003210.1/1958601-1958511 Listeria monocytogenes strain EGD
NC_004193.1/760480-760571 Oceanobacillus iheyensis
NC_004193.1/769695-769781 Oceanobacillus iheyensis
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NC_004193.1/1103947-1104044 Oceanobacillus iheyensis
NC_002745.1/430771-430861 Staphylococcus aureus subsp. aureus
NC_004461.1/2432384-2432294 Staphylococcus epidermidis
NC_004116.1/1093950-1093860 Streptococcus agalactiae
NC_002737.1/930757-930842 Streptococcus pyogenes
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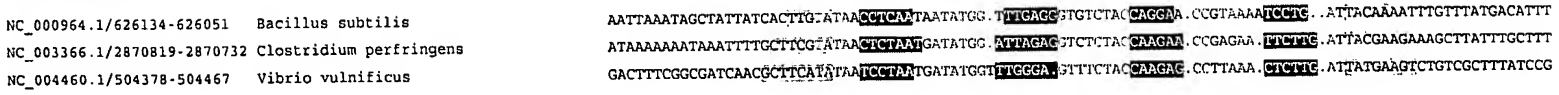
NC_003869.1/586372-586463 Thermoanaerobacter tengcongensis
Consensus

D. A-Box


NC_000964.1/626134-626051 Bacillus subtilis
NC_003366.1/2870819-2870732 Clostridium perfringens
NC_004460.1/504378-504467 Vibrio vulnificus

E. Lysine riboswitch comparison

Command-1 Plain Text

Command-2 Base paired stem 1

Command-3 Base paired stem 2

i. Command-4 Base paired stem 3

Command-5 Base paired stem 4

Command-6 Base paired stem 5

ii. [redacted]

Command-8 Terminator poly-U

Command-9 Downstream AT stem paired to stem 1

Command-0 Optional base paired stem 2

CUAG is 90% sequence similarity

2. **CUAG is the Anti-Terminator**

CUAG is the Terminator stem